

GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: December 7, 2005, 23:55:46 ; Search time 2057 Seconds
(without alignment)
4393.830 Million cell updates/sec

Title: US-10-691-412-1
Perfect score: 159
Sequence: 1 atggagaaagtcacacac.....tcacgtgatgcttctga 159

Scoring table: IDENTITY NUC
Gapop 10.0 , Gapext 1.0

Searched: 5983141 seqs, 28421725653 residues

Total number of hits satisfying chosen parameters: 11766282

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 100 summaries

Database : GenEmbl.*

1: gb_ba.*
2: gb_in.*
3: gb_env.*
4: gb_om.*
5: gb_ov.*
6: gb_pat.*
7: gb_ph.*
8: gb_pr.*
9: gb_ro.*
10: gb_sts.*
11: gb_sy.*
12: gb_un.*
13: gb_vl.*
14: gb_htg.*
15: gb_pl.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	159	100.0	323	8	HUMPLAM
2	159	100.0	480	6	BD030469
3	159	100.0	480	6	AX894936
4	159	100.0	980	8	HSPLBG2
5	159	100.0	1635	6	CQ178671
6	159	100.0	1635	6	AX329653
7	159	100.0	1635	8	HUMPHLAM
8	159	100.0	1691	8	BC005269
9	159	100.0	1712	6	CS115190
10	159	100.0	60797	14	ALJ35356
11	159	100.0	60992	14	ALJ35356
12	159	100.0	150290	8	HS509L4
13	144.6	90.9	159	6	BD247911
14	144.6	90.9	159	6	AR302007
15	144.6	90.9	159	6	AX040491
16	144.6	90.9	858	4	RASPFLAM2
17	143	89.9	159	6	BD247907
18	143	89.9	159	6	AR302003

19	143	89.9	159	6	AX040487
20	143	89.9	737	4	SSPLB
21	143	89.9	2841	4	OCPLAM
22	139.8	87.9	314	4	AY514751
23	139.8	87.9	669	4	AY576871S2
24	139.8	87.9	832	4	DOGPHL
25	139.8	87.9	832	4	DOGPHL
26	139.8	87.9	2614	4	CFPHLX
27	135.2	85.0	179556	14	AC013809
28	128.6	80.9	648	9	BC061097
29	128.6	80.9	940	9	S46792
30	128.6	80.9	167574	9	AC153524
31	127.6	80.3	306	6	CQ447405
32	127	79.9	79895	14	AC100317
33	125.4	78.9	159	9	S95853
34	125.4	78.9	386	9	S95849
35	125.4	78.9	1786	9	RATPHOLA02
36	125.4	78.9	223728	14	AC097906
37	125.4	78.9	231910	14	AC128365
38	123.8	77.9	701	9	RNPHLAM
39	109.4	68.8	332	5	CHKPLB
40	109.4	68.8	3423	5	CHKPLB2
41	83	52.2	315	6	AR121629
42	74.2	46.7	132837	5	CR926459
43	74.2	46.7	133901	5	BS537355
44	71	44.7	130240	5	BS276081
45	41.4	26.0	179556	14	AC013809
46	36.8	23.1	134286	8	AC025771
47	36.8	23.1	170272	8	AC024589
48	36.4	22.9	116103	8	AL590653
49	35.8	22.5	136485	14	AC158428
50	35.4	22.3	141913	8	AL512452
51	35.4	22.3	144134	8	HS183K14
52	35.4	22.3	170640	14	AC164940
53	35.2	22.1	96013	8	AB042236
54	35.2	22.1	126334	14	AL133403
55	35.2	22.1	156978	8	AP002531
56	35	22.0	69973	14	AC095088_4
57	35	22.0	99545	14	AC094905_4
58	35	22.0	101678	14	CT009608
59	35	22.0	110000	14	AC094905_3
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62	35	22.0	175664	5	AL833789_6
63	35	22.0	269409	14	AC109577
64	35	22.0	274103	14	CR847827
65	35	22.0	312853	14	AC118393
66	34.8	21.9	3994	5	CR762494
67	34.8	21.9	143819	14	AC137765
68	34.8	21.9	151900	8	AC096644
69	34.8	21.9	165839	14	AC162119
70	34.8	21.9	165790	4	BX088590
71	34.8	21.9	167346	8	AC096640
72	34.8	21.9	167898	14	AC110891
73	34.8	21.9	178371	5	BX005174
74	34.8	21.9	189510	5	CR391977
75	34.8	21.9	212443	14	AL772323
76	34.8	21.9	251443	9	AC096251
77	34.6	21.8	2043	6	BD085809
78	34.6	21.8	2060	8	AF078533
79	34.6	21.8	227788	14	AC095653
80	34.6	21.8	232042	14	AC128144
81	34.6	21.8	246335	14	AC109060
82	34.6	21.8	247254	14	AC114844
83	34.4	21.6	167510	9	AC144773
84	34.4	21.6	239028	14	AC111814
85	34.4	21.6	246901	14	AC108350
86	34.4	21.6	249125	14	AC162916
87	34.4	21.6	263578	14	AC015657
88	34.2	21.5	805	10	BV054436
89	34.2	21.5	59744	14	AC103989
90	34.2	21.5	76233	14	CR974465
91	34.2	21.5	85025	9	AL683799

AX040487	Sequence
X15075	Pig mRNA fo
Y00761	O.cuniculus
AY514751	Canis fam
AY576871S2	Canis fam
M16012	Canine card
M35393	Dog cardioc
Y00399	Dog phospho
BC061097	Homo sapi
S46792	phospholamb
AC153524	Mus muscu
CQ447405	Sequence
AC100317	Mus muscu
S95853	phospholamb
S95849	Rattus sp.
L03382	Rat phospho
AC097906	Rattus no
AC128365	Rattus no
X1088	R.norvegicu
MS9039	Chicken car
MS9038	Chicken pho
AR121629	Sequence
CR926459	Zebrafish
BS537355	Zebrafish
BS276081	Zebrafish
AC013809	Homo sapi
AC025771	Homo sapi
AC024589	Homo sapi
AL590653	Human DNA
AL158428	Ornithorh
AL512452	Human DNA
AL109913	Human DNA
AC164940	Atelerix
AB042236	Homo sapi
AL133403	Homo sapi
AP002531	Homo sapi
Continuation (5 of	
Continuation (5 of	
CT009608	Danio rer
Continuation (4 of	
Continuation (7 of	
Continuation (7 of	
AL833789	Zebrafish
AC109577	Rattus no
CR847827	Danio rer
AC118393	Rattus no
CR762494	Zebrafish
AC137765	Mus muscu
AC096644	Homo sapi
AC162119	Pig DNA s
BX088590	Cercopith
AC096640	Homo sapi
AC110891	Mus muscu
BX005174	Zebrafish
CR391977	Zebrafish
AL772323	Mouse DNA
AC096251	Rattus no
BD085809	Caspase-1
AF078533	Homo sapi
AC095653	Rattus no
AC128144	Rattus no
AC109060	Rattus no
AC114844	Rattus no
AC144773	Mus muscu
AC111814	Rattus no
AC108350	Rattus no
AC162916	Mus muscu
AC015657	Mus muscu
BV054436	S212P6052
AC103989	Homo sapi
CR974465	Mouse DNA
AL683799	Mouse DNA

92 34.2 21.5 125804 14 AC019853 Drosophil
93 34.2 21.5 162288 14 AL731730 Mus muscu
c 94 34.2 21.5 162288 14 AL731730 Mus muscu
95 34.2 21.5 163514 2 AC091227 Drosophil
c 96 34.2 21.5 165318 2 AC010061 Drosophil
97 34.2 21.5 168977 9 AL844838 Mouse DNA
c 98 34.2 21.5 175208 9 AC112156 Mouse DNA
99 34.2 21.5 175976 9 AC132593 Mus muscu
c 100 34.2 21.5 176697 14 AC104413 Mus muscu

ALIGNMENTS

RESULT 1
LOCUS HUMPLAM 323 bp mRNA linear PRI 07-JAN-1995
DEFINITION Human phospholamban mRNA, complete cds.
ACCESSION M60411
VERSION M60411.1 GI:190018
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Hominiidae; Homo.
REFERENCE 1 (bases 1 to 323)
AUTHORS Salvatore, C.A. and Jacobson, M.A.
TITLE Cloning of human cardiac phospholamban
JOURNAL Unpublished (1991)
COMMENT Original source text: Human heart, cDNA to mRNA.

FEATURES
source
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ORIGIN
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Best Local Similarity 100.0%; Pred. No. 8.6e-32;
Matches 159; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 ATGGAGAAAGTCCAAATACCTCAGCTCAGCTATAGAGAGCCTCAACCAATTGAATG 60
Db 75 ATGGAGAAAGTCCAAATACCTCAGCTCAGCTATAGAGAGCCTCAACCAATTGAATG 134
QY 61 CCTCAACAGCAGCTCAAAAGCTACAGAATCTATTATCAATTTCTGCTCATCTTAATA 120
Db 135 CCTCAACAGCAGCTCAAAAGCTACAGAATCTATTATCAATTTCTGCTCATCTTAATA 194
QY 121 TGTCTCTTGTGATCTGTATCATCGTATGATGCTTCTCTGA 159
Db 195 TGTCTCTTGTGATCTGTATCATCGTATGATGCTTCTCTGA 233

RESULT 2
LOCUS BD030469 480 bp DNA linear PAT 27-AUG-2002
DEFINITION Sequence tag and encoded human protein.
ACCESSION BD030469

VERSION BD030469.1 GI:22572211
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Hominiidae; Homo.
REFERENCE 1 (bases 1 to 480)
AUTHORS Edwards, J.B.D.M., Duclair, E. and Jordan, J.Y.
TITLE Sequence tag and encoded human protein
JOURNAL Patent: JP 2001269182-A 6715 02-OCT-2001;
GENSET

COMMENT
OS Homo sapiens (human)
PN JP 2001269182-A/6715
PD 02-OCT-2001
PF 24-FEB-2000 JP 2000118773
PR 26-FEB-1999 US 60/122487
PI JEAN BAPTISTE DUMAS MILNE EDWARDS, EIMERIC DUCLAIR, JEAN YVES
PC C12N15/09, C07K14/435, C07K16/18, C12N1/15, C12N1/19, C12N1/21, PC
C12N5/10,
PC C12P21/02, C12P21/08, C12Q1/68//G06F17/30, C12N15/00, C12N5/00, PC
G06F15/40

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Best Local Similarity 100.0%; Pred. No. 8.1e-32;
Matches 159; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 ATGGAGAAAGTCCAAATACCTCAGCTCAGCTATAGAGAGCCTCAACCAATTGAATG 60
Db 196 ATGGAGAAAGTCCAAATACCTCAGCTCAGCTATAGAGAGCCTCAACCAATTGAATG 255
QY 61 CCTCAACAGCAGCTCAAAAGCTACAGAATCTATTATCAATTTCTGCTCATCTTAATA 120
Db 256 CCTCAACAGCAGCTCAAAAGCTACAGAATCTATTATCAATTTCTGCTCATCTTAATA 315
QY 121 TGTCTCTTGTGATCTGTATCATCGTATGATGCTTCTCTGA 159
Db 316 TGTCTCTTGTGATCTGTATCATCGTATGATGCTTCTCTGA 354

RESULT 3
LOCUS AX894936 480 bp DNA linear PAT 18-DEC-2003
DEFINITION Sequence 10799 from Patent EP1033401.
ACCESSION AX894936
VERSION AX894936.1 GI:40049820
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Hominiidae; Homo.

REFERENCE 1
AUTHORS Dumas Milne Edwards, J.B., Duclert, A. and Giordano, J.Y.
TITLE Express sequence tags and encoded human proteins
JOURNAL Patent: EP 1033401-A 10799 06-SEP-2000;
GENSET (FR)
FEATURES
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ORIGIN

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Dd	196	ATGCAGAAAGTCCCAATACCTCAGTCGCTACGCTATAGAAGAGGCTCAACCAATGAAATG	255	
Qy	61	CCTCAACAAGCAGCGTCAAAAAGCTACAGAATCTATTATCAATTTCTGTCTCATCTTTAATA	120	
Dd	256	CCTCAACAAGCAGCGTCAAAAAGCTACAGAATCTATTATCAATTTCTGTCTCATCTTTAATA	315	
Qy	121	TGTCCTTTGCTGATCTGTATCATCGTGATGCTCTCTGA	159	
Dd	316	TGTCCTTTGCTGATCTGTATCATCGTGATGCTCTCTGA	354	
RESULT 4				
HSPLEB2				
LOCUS		980 bp	DNA	linear PRI 21-SEP-1999
DEFINITION		Homo sapiens phospholamban gene, exon 2 and complete cds.		
ACCESSION		AF177764		
VERSION		AF177764.1	GI:5916236	
KEYWORDS				
SEGMENT		2 of 2		
SOURCE		Homo sapiens (human)		
ORGANISM		Homo sapiens		
		Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;		
		Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;		
		Hominidae; Homo.		
REFERENCE				
AUTHORS		McTiernan, C.F., Frye, C.S., Lemster, B.H., Kinder, E.A.,		
		Ogletree-Hughes, M.L., Moravec, C.S. and Feldman, A.M.		
TITLE		The human phospholamban gene: structure and expression		
JOURNAL		J. Mol. Cell. Cardiol. 31 (3), 679-692 (1999)		
PUBMED		10198197		
REFERENCE		2 (bases 1 to 980)		
AUTHORS		McTiernan, C.F., Frye, C.S., Lemster, B.H., Kinder, E.A.,		
		Ogletree-Hughes, M.L., Moravec, C.S. and Feldman, A.M.		
TITLE		Direct Submission		
JOURNAL		Submitted (16-AUG-1999) Cardiovascular Institute, University of		
		Pittsburgh, 200 Lothrop St., Pittsburgh, PA 15213, USA		
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Best Local Similarity		100.0%;	Pred. No. 7.3e-32;	Length 980;
Matches 159;		Conservative 0;	Mismatches 0;	Indels 0;
Gaps 0;				
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Dd	132	ATGCAGAAAGTCCCAATACCTCAGTCGCTATAGAAGAGGCTCAACCAATGAAATG	191	
Qy	61	CCTCAACAAGCAGCGTCAAAAAGCTACAGAATCTATTATCAATTTCTGTCTCATCTTTAATA	120	
Dd	192	CCTCAACAAGCAGCGTCAAAAAGCTACAGAATCTATTATCAATTTCTGTCTCATCTTTAATA	251	

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CDS

ORIGIN

Query Match 100.0%; Score 159; DB 8; Length 1691;
Best Local Similarity 100.0%; Pred. No. 6.8e-32;
Matches 159; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db 163 ATGGAGAAGTCCATACCTCAGCTCAGCTATAGAAGAGCTCAACCATTTGAATG 222
Qy 61 CCTCAACAGCAGTCAAAAGCTACAGATCTATTATCAATTTCTCTCATCTTAATA 120
Db 223 CCTCAACAGCAGTCAAAAGCTACAGATCTATTATCAATTTCTCTCATCTTAATA 282
Qy 121 TGTCTCTTGTGATCTGTATCATCGTATGCTTCTCTGA 159
Db 283 TGTCTCTTGTGATCTGTATCATCGTATGCTTCTCTGA 321

RESULT 9
LOCUS CS115190 1712 bp DNA linear PAT 08-JUL-2005
DEFINITION Sequence 1 from Patent EP1548131.
ACCESSION CS115190
VERSION CS115190.1 GI:70663800
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Hominidae; Homo.

REFERENCE 1
AUTHORS Clerc, R.G., Duchateau-Nguyen, G., Gardes, C., Mizrahi, J. and Ostenson, C.G.
TITLE Novel targets for obesity from skeletal muscle
JOURNAL Patent: EP 1548131-A 1 29-JUN-2005;
F. Hoffmann-La Roche AG (CH); Claes-Goran Ostenson (SE)
FEATURES
source Location/Qualifiers
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ORIGIN

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Best Local Similarity 100.0%; Pred. No. 6.8e-32;
Matches 159; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 ATGGAGAAGTCCATACCTCAGCTCAGCTATAGAAGAGCTCAACCATTTGAATG 60
Db 182 ATGGAGAAGTCCATACCTCAGCTCAGCTATAGAAGAGCTCAACCATTTGAATG 241
Qy 61 CCTCAACAGCAGTCAAAAGCTACAGATCTATTATCAATTTCTCTCATCTTAATA 120
Db 242 CCTCAACAGCAGTCAAAAGCTACAGATCTATTATCAATTTCTCTCATCTTAATA 301
Qy 121 TGTCTCTTGTGATCTGTATCATCGTATGCTTCTCTGA 159

Db

RESULT 10
AL355356
LOCUS
DEFINITION
ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM

AL355356 60797 bp DNA linear HTG 13-JUN-2001
Homo sapiens chromosome 6 clone RP11-411H20, 19 unordered pieces.

AL355356 GI:9930900
HTG; HTGS PHASE1; HTGS_CANCELLED.
Homo sapiens (human)

Homo sapiens
Eukaryota; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Hominidae; Homo.

REFERENCE
AUTHORS
TITLE
JOURNAL

1 Sims, S.

Direct Submission

Submitted (12-JUN-2001) Sanger Centre, Hinxton, Cambridgeshire,
CB10 1SA, UK. E-mail enquiries: humquery@sanger.ac.uk
requests: clonerrequest@sanger.ac.uk
On Aug 27, 2000 this sequence version replaced gi:9800876.

COMMENT

----- Genome Center

Center: Sanger Centre

Center code: SC

Web site: http://www.sanger.ac.uk

Contact: humquery@sanger.ac.uk

----- Project Information

Center project name: BA411H20

----- Summary Statistics

Assembly program: XGAP4; version 4.5

Sequencing vector: plasmid; L08752; 100% of reads

Chemistry: Dye-terminator Big Dye; 100% of reads

Consensus quality: 44913 bases at least Q40

Consensus quality: 51172 bases at least Q30

Consensus quality: 54968 bases at least Q20

Insert size: 58997; sum-of-contigs

Insert size: 149898; 19.4% error; agarose-fp

Quality coverage: 1.67x in Q20 bases; sum-of-contigs Quality

coverage: 1.06x in Q20 bases; agarose-fp

***** NOTE: This is a 'working draft' sequence. It currently
* consists of 19 contigs. The true order of the pieces
* is not known and their order in this sequence record is
* arbitrary. Gaps between the contigs are represented as
* runs of N, but the exact sizes of the gaps are unknown.
* This record will be updated with the finished sequence.
* as soon as it is available and the accession number will
* be preserved.

1 2490: contig of 2490 bp in length
* 2491 2590: gap of 100 bp
* 2591 6525: contig of 3935 bp in length
* 6526 6625: gap of 100 bp
* 6626 12056: contig of 5431 bp in length
* 12057 12156: gap of 100 bp
* 12157 17566: contig of 5410 bp in length
* 17567 17666: gap of 100 bp
* 17667 20601: contig of 2935 bp in length
* 20602 20701: gap of 100 bp
* 20702 23770: contig of 3069 bp in length
* 23771 23870: gap of 100 bp
* 23871 26583: contig of 2713 bp in length
* 26584 29566: contig of 2883 bp in length
* 29567 29666: gap of 100 bp
* 29667 32061: contig of 2395 bp in length
* 32062 32161: gap of 100 bp
* 32162 34362: contig of 2201 bp in length
* 34363 34463: gap of 100 bp
* 34463 37698: contig of 3236 bp in length
* 37699 37798: gap of 100 bp
* 37799 42053: contig of 4255 bp in length

Fri Dec 9 12:22:30 2005

* 42054 42153: gap of 100 bp
* 42154 44594: contig of 2441 bp in length
* 44595 44694: gap of 100 bp
* 44695 48031: contig of 3337 bp in length
* 48032 48131: gap of 100 bp
* 48132 50319: contig of 2188 bp in length
* 50320 50419: gap of 100 bp
* 50420 53189: contig of 2770 bp in length
* 53190 53289: gap of 100 bp
* 53290 55344: contig of 2055 bp in length
* 55345 55444: gap of 100 bp
* 55445 57739: contig of 2295 bp in length
* 57740 57839: gap of 100 bp
* 57840 60797: contig of 2958 bp in length.
FEATURES
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/clone_lib="RPC1-11.2"
1. .2490
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fragment_chain:1"
2591. .6525
/note="assembly fragment:00003
fragment_chain:1"
6626. .12056
/note="assembly fragment:00133
fragment_chain:2"
12157. .17566
/note="assembly fragment:00093
fragment_chain:2"
17667. .20601
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20702. .23770
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23871. .26583
/note="assembly fragment:00022"
26684. .29566
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29667. .32061
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32162. .34362
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34463. .37698
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37799. .42053
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42154. .44594
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44695. .48031
/note="assembly fragment:00324"
48132. .50319
/note="assembly fragment:00340"
50420. .53189
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53290. .55344
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55445. .57739
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57840. .60797
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ORIGIN

Query Match 100.0%; Score 159; DB 14; Length 60797;
Best Local Similarity 100.0%; Pred. No. 4.1e-32;
Matches 159; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 ATGGAGAAAGTCCAAATACCTCGCTCAGCTATAGAAGAGCTCAACCAATGAAATG 60

Db 19706 ATGGAGAAAGTCCAAATACCTCGCTCAGCTATAGAAGAGCTCAACCAATGAAATG 19765
Qy 61 CCTCAACAAGCAGCGTCAAAAGCTACAGAATCTATTATCAATTTCTGTCTCATCTTAATA 120
Db 19766 CCTCAACAAGCAGCGTCAAAAGCTACAGAATCTATTATCAATTTCTGTCTCATCTTAATA 19825
Qy 121 TGTCTTGTGTGATCTGTATCATCGTGATGCTTCTCTGA 159
Db 19826 TGTCTTGTGTGATCTGTATCATCGTGATGCTTCTCTGA 19864
RESULT 11
ALL36974 66092 bp DNA linear HTG 10-JUL-2001
LOCUS Homo sapiens chromosome 6 clone RP3-436C16, 2 unordered pieces.
DEFINITION ALL36974
ACCESSION ALL36974 GI:9930800
VERSION ALL36974.4 GI:9930800
KEYWORDS HTG; HTGS PHASE1; HTGS_CANCELLED.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Hominidae; Homo.
1
REFERENCE
AUTHORS Williams,S.
TITLE Direct Submission
JOURNAL Submitted (09-JUL-2001) Sanger Centre, Hinxton, Cambridgeshire,
CB10 1SA, UK. E-mail enquiries: humquery@sanger.ac.uk
requests: clonerquest@sanger.ac.uk
On Aug 27, 2000 this sequence version replaced gi:9863476.
COMMENT
----- Genome Center
Center: Sanger Centre
Center code: SC
Web site: http://www.sanger.ac.uk
Contact: humquery@sanger.ac.uk
----- Project Information
Center project name: dJ436C16
----- Summary Statistics
Assembly program: XGAP4; version 4.5
Sequencing vector: plasmid; L08752; 100% of reads
Chemistry: Dye-terminator Big Dye; 100% of reads
Consensus quality: 65294 bases at least Q40
Consensus quality: 65764 bases at least Q30
Consensus quality: 65936 bases at least Q20
Insert size: 65992; sum-of-contigs
Insert size: 77256; 1.8% error; agarose-fp
Quality coverage: 8.00x in Q20 bases; sum-of-contigs Quality
coverage: 7.55x in Q20 bases; agarose-fp

* NOTE: This is a 'working draft' sequence. It currently
* consists of 2 contigs. The true order of the pieces
* is not known and their order in this sequence record is
* arbitrary. Gaps between the contigs are represented as
* runs of N, but the exact sizes of the gaps are unknown.
* This record will be updated with the finished sequence
* as soon as it is available and the accession number will
* be preserved.
* 1 63797: contig of 63797 bp in length
* 63798 63897: gap of 100 bp
* 63898 66092: contig of 2195 bp in length.
FEATURES
source
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1. .66092
/organism="Homo sapiens"
/mol_type="genomic DNA"
/db_xref="taxon:9606"
/chromosome="6"
/clone="RP3-436C16"
/clone_lib="RPC1-3"
1. .63797
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63898. .66092
/note="assembly fragment:01022"

• ORIGIN

Query Match 100.0%; Score 159; DB 14; Length 66092;
 Best Local Similarity 100.0%; Pred. No. 4e-32;
 Matches 159; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ATGAGAGAAAGTCCAAATACCTCAGCTCAGCTATAGAGAGGCTCAACATTGAAATG 60
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 Db 10299 ATGAGAGAAAGTCCAAATACCTCAGCTCAGCTATAGAGAGGCTCAACATTGAAATG 10358
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QY 61 CCTCAACAGCAGCTCAAAAGCTACAGATCTATTATCAATTTCTCTCTCATCTTAATA 120
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 Db 10359 CCTCAACAGCAGCTCAAAAGCTACAGATCTATTATCAATTTCTCTCTCATCTTAATA 10418
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QY 121 TGTCTTCTGATCTGTATCATGCTGATGCTTCTCTGA 159
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 Db 10419 TGTCTTCTGATCTGTATCATGCTGATGCTTCTCTGA 10457
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RESULT 12

HS09L4/c

LOCUS

DEFINITION

HS09L4 150290 bp DNA linear PRI 18-MAY-2005
 Human DNA sequence from clone RP3-509L4 on chromosome 6q22.1-22.33
 Contains part of the gene for serologically defined breast cancer
 antigen NY-BR-15 (LOC221312), the PLN gene for phospholamban (PLB),
 a bromodomain-containing 7 (BRD7) pseudogene and a synovial sarcoma
 X breakpoint gene pseudogene, complete sequence.

ACCESSION

VERSION

KEYWORDS

SOURCE

ORGANISM

REFERENCE

AUTHORS

TITLE

JOURNAL

COMMENT

FEATURES

SOURCE

FEATURES

SOURCE

FEATURES

SOURCE

FEATURES

SOURCE

FEATURES

SOURCE

FEATURES

SOURCE

FEATURES

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FEATURES

/db_xref="taxon:9606"
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 /clone="RP3-509L4"
 /clone_lib="RPC1-3"
 /complement(34236..34800)
 /locus_tag="RP3-509L4.1-001"
 /pseudo
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 /locus_tag="RP3-509L4.1-001"
 /notes="match: proteins: AAH01003 AAH05325 AAH16957 O60224
 O60225 O75101 Q16384 Q16385 Q8W29 Q96W3 Q96I7 Q96Q10
 Q96Q11 Q99909 Q9BRW7 Q9BU88 Q9CPUI Q9NZK4 Q9Y444"
 /codon_start=1
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 /locus_tag="RP11-57K17.2-006"
 /join(49802..49879,57554..58311)
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 /locus_tag="RP11-57K17.2-006"
 /notes="match: ESTs: BE784038"
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 99950..100068,112455..112572,132005..132184,
 140012..140164,141937..142091,143357..143474,
 143949..143999,complement(AL589993.5:93104..93211),
 complement(AL589993.5:91639..91870),
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 /locus_tag="RP11-57K17.2-001"
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 140012..140164,141937..142091,143357..143474,
 143949..143999,complement(AL589993.5:93104..93211),
 complement(AL589993.5:91639..91870),
 complement(AL589993.5:83339..88135))
 /gene="RP11-57K17.2"
 /locus_tag="RP11-57K17.2-001"
 /notes="match: ESTs: AA383216 AA459978 AA741093 AA856722
 AA938309 AA948449 AI377047 AI635527 AI660060 AI761092
 AL110424 AV0319271 AV158613 AV161104 AV162723 AW022132
 AW081116 AW294514 AW510803 AW593214 AW598301 BB312808
 BB634052 BE000305 BE784038 BF592294 BF740910 B1519961
 B1830115 B1857240 BM364523 BM365596 BM365622 BM365636
 BM540451 BM682243 BM723381 BM724601 BM803234 BM952538
 BQ038529
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 99950..100068,112455..112572,132005..132184,
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 143949..143999,complement(AL589993.5:93104..93211),
 complement(AL589993.5:91639..91870),
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 Q9UF52"
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 /translation="MWGFLAPEAGSRDPGARSFPAGPDYSSAWLPAWELWATTT
 VPSNRNHHIRHSIASDGTGTCSDSVSDHSTSGTSLTGLTPTAHV
 MPSSASISKRLRSIATPDGKSWTSLMQLGNHSGDQSLDKMDKPRKRWKSL
 KLTAPDNCGGTVCRESNRKLEKIGAKALTQRTIGPSCLHDSMLRLEKEL
 NKTGSSTLDCKYKFECSKEDFRASSSTLRQPDVMTYSALPESKPIWTSSEAPPPK
 YMLGQQAAGVGIQPSVRTQWLTQRTNPLEGNTEDSYSLAPWQQQLDPRQG
 SETPMQVLTGSSRSYSGYQDFSKWESMLIKSGLLRQKEIVIDRQQLTHLHERI
 RDNELRAQHAWLGHVNCDSIVASLPQYENTSLQTPFSESVSHSQQGFQKLIAS

This sequence was finished as follows unless otherwise noted: all
 regions were either double-stranded or sequenced with an alternate
 chemistry or covered by high quality data (i.e., phred quality >= 30); an attempt was made to resolve all sequencing problems, such
 as compressions and repeats; all regions were covered by at least
 one subclone; and the assembly was confirmed by restriction digest,
 except on the rare occasion of the clone being a YAC.

FEATURES

Location/Qualifiers

1..150290
 /organism="Homo sapiens"
 /mol_type="genomic DNA"
 /db_xref="RZPD:RPCIP704L04509"

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ETLEKYLADLPTLDVOSQSLQLOILEBKNLQEOALIDTEKKLEIKKQCODKETOL
ICQKKEKELVTVQSLQOKVERCLEGIRLPMLDKOLQENENLNROONETASKIID
SQOEDIRMIILEISQMKJLSEKELTTQKMEELEKERNVORLTKALLEINQROCTDE
CSLDQGGEPQSQOQTVLSKRPLFDLVIDOLFKEMSCCLFDLKALCSILNQRAQK
EPNLSLLGIRSMNGSASETENDSHSTETLTKKLSDVCCQLRRDIDELRTTISDRYAQM
GDNLCITO"
join(complement(AL390069.9:40642..40752),
complement(AL390069.9:28931..29039),
complement(AL390069.9:8684..8842),57554..>57944)
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complement(AL390069.9:8684..8842),57554..>57944)
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ATTVPSNRRNHRHSIASDGTIGTSCSDVEDHSTSGTILSFPSQSLTLP
AHWPSNSASISKLRESLTPDGSKWSLTMQTLGNHSGEQDSSLDKDFPLRKWS
SLSKLTAPNCCGGTVCREERNGLEKIGAKALTSQRLTIGPSCLDS"
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/locus tag="RP11-57K17.2-002"
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complement(AL390069.9:8684..8842),57554..>57815)
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/locus tag="RP11-57K17.2-002"
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complement(AL390069.9:8684..8842),57554..>57778)
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complement(AL390069.9:8684..8842),57554..>57778)
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57628..>57815
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MKDFRPLRKWSLSKLTAP"
57628..>57778
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Best Local Similarity 100.0%; Pred. No. 3.6e-32;
Matches 159; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 ATGAGAAAAGTCCAATACCTCAGTCAGCTATAGAAGAGCCTCAACCATTTGAATG 60
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Db 64948 ATGAGAAAAGTCCAATACCTCAGTCAGCTATAGAAGAGCCTCAACCATTTGAATG 64889
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QY 61 CCTCAAGACGACCTCAAAAGCTACAGAACTATTATTCAATTTCTGTCTCATCTTAATA 120
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Db 64888 CCTCAAGACGACCTCAAAAGCTACAGAACTATTATTCAATTTCTGTCTCATCTTAATA 64829
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QY 121 TGTCTCTTGTGATCTGTATCATCGTGTATGCTTCTCTGA 159
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Db 64828 TGTCTCTTGTGATCTGTATCATCGTGTATGCTTCTCTGA 64790
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RESULT 13
BD247911
LOCUS 159 bp DNA linear PAT 17-JUL-2003
DEFINITION Method for screening compounds.
ACCESSION BD247911
VERSION BD247911.1 GI:33057681
KEYWORDS JP 2002541859-A/13.
SOURCE synthetic construct
ORGANISM synthetic construct
other sequences; artificial sequences.
REFERENCE 1 (bases 1 to 159)
AUTHORS Zwaal, R., Groenen, J. and Bogaert, T.
TITLE Method for screening compounds
JOURNAL Patent: JP 2002541859-A 13 10-DEC-2002;
DEVGEN NV
COMMENT OS Artificial Sequence
PN JP 2002541859-A/13
PD 10-DEC-2002
PF 14-APR-1999 GB 9908670.4,15-APR-1999 US 60/129596 PR
PR 15-APR-1999 GB 9912736.7
PI 01-JUN-1999 GB
PI RICHARD ZWAAL,JOSE GROENEN,THIERRY BOGAERT
PC C12Q1/42,C12N15/09,C12Q1/02,C12N15/00
CC Description of Artificial Sequence:HUMANIZED BIG PLB CDNA FH
Key Location/Qualifiers
FT source 1..159
FT /organism='Artificial Sequence'.
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source Location/Qualifiers
1..159
/organism="synthetic construct"
/mol_type="genomic DNA"
/db_xref="taxon:32630"
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Best Local Similarity 94.3%; Pred. No. 6.4e-28;
Matches 150; Conservative 0; Mismatches 9; Indels 0; Gaps 0;
QY 1 ATGAGAAAAGTCCAATACCTCAGTCAGCTATAGAAGAGCCTCAACCATTTGAATG 60
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Db 1 ATGAGAAAAGTCCAATACCTCAGTCAGCTATAGAAGAGCCTCAACCATTTGAATG 60
|||||
QY 61 CCTCAAGACGCTCAAAACCTTCAGAACCTATTATTCAATTTCTGTCTCATCTTAATA 120
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Db 61 CCTCAAGACGCTCAAAACCTTCAGAACCTATTATTCAATTTCTGTCTCATCTTAATA 120
|||||
QY 121 TGTCTCTTGTGATCTGTATCATCGTGTATGCTTCTCTGA 159
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Db 121 TGCCTCTTGTGATTTGTCATCATCGTGTATGCTTCTCTGA 159
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RESULT 14
AR302007

LOCUS AR302007 159 bp DNA linear PAT 12-JUN-2003
DEFINITION Sequence 13 from patent US 6540996.
ACCESSION AR302007
VERSION AR302007.1 GI:31689912
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 159)
AUTHORS Zwaal,R., Groenen,J. and Bogaert,T.
TITLE Compound screening methods
JOURNAL Patent: US 6540996-A 13 01-APR-2003;
Devgen NV; Ghent-Zwijnaarde;
GBX;
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source Location/Qualifiers
1..159
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ORIGIN
Query Match 90.9%; Score 144.6; DB 6; Length 159;
Best Local Similarity 94.3%; Pred. No. 6.4e-28;
Matches 150; Conservative 0; Mismatches 9; Indels 0; Gaps 0;
QY 1 ATGGAGAAGTCCAAATACCTCACTCGCTCAGCTATAGAAGAGCCTCAACCAATTGAAATG 60
Db 1 ATGGAGAAGTCCAAATACCTCACTCGCTCAGCTATAGAAGAGCCTCAACCAATTGAAATG 60
QY 61 CCTCAACAGCAGCTCAAAAGCTACAGATCTATTATCAATTTCTGCTCATCTTAATA 120
Db 61 CCTCAACAGCAGCTCAAAAGCTACAGATCTATTATCAATTTCTGCTCATCTTAATA 120
QY 121 TGTCTCTTGTGATCTGTATCATCGTATGCTTCTCTGA 159
Db 121 TGCCTCTTGTGATTTGTCATCATCGTATGCTTCTCTGA 159
RESULT 15
AX040491
LOCUS AX040491 159 bp DNA linear PAT 18-NOV-2000
DEFINITION Sequence 13 from Patent WO0063426.
ACCESSION AX040491
VERSION AX040491.1 GI:11230280
KEYWORDS
SOURCE synthetic construct
ORGANISM synthetic construct
other sequences; artificial sequences.
REFERENCE 1
AUTHORS Zwaal,R., Groenen,J. and Bogaert,T.
TITLE Compound screening methods
JOURNAL Patent: WO 0063426-A 13 26-OCT-2000;
Devgen NV (BE)
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source Location/Qualifiers
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/db_xref="taxon:32630"
/note="HUMANIZED PIG PLB CDNA"
ORIGIN
Query Match 90.9%; Score 144.6; DB 6; Length 159;
Best Local Similarity 94.3%; Pred. No. 6.4e-28;
Matches 150; Conservative 0; Mismatches 9; Indels 0; Gaps 0;
QY 1 ATGGAGAAGTCCAAATACCTCACTCGCTCAGCTATAGAAGAGCCTCAACCAATTGAAATG 60
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QY 61 CCTCAACAGCAGCTCAAAAGCTACAGATCTATTATCAATTTCTGCTCATCTTAATA 120
Db 61 CCTCAACAGCAGCTCAAAAGCTACAGATCTATTATCAATTTCTGCTCATCTTAATA 120
QY 121 TGTCTCTTGTGATCTGTATCATCGTATGCTTCTCTGA 159

Db 121 TGCCTCTTGTGATTTGTCATCATCGTATGCTTCTCTGA 159
RESULT 16
RABPHLAM2
LOCUS RABPHLAM2 858 bp DNA linear MAM 27-APR-1993
DEFINITION Rabbit phospholamban gene, partial exon 2.
ACCESSION M3601
VERSION M3601.1 GI:165636
KEYWORDS phospholamban.
SEGMENT 2 of 3
SOURCE Oryctolagus cuniculus (rabbit)
ORGANISM Oryctolagus cuniculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Glires; Lagomorpha;
Leporidae; Oryctolagus.
REFERENCE 1 (bases 1 to 858)
AUTHORS Fujii,J., Zarain-Herzberg,A., Willard,H.F., Tada,M. and
MacLennan,D.H.
TITLE Structure of the rabbit phospholamban gene, cloning of the human
cDNA, and assignment of the gene to human chromosome 6
JOURNAL J. Biol. Chem. 266 (18), 11669-11675 (1991)
PUBMED 1828805
COMMENT Original source text: Rabbit DNA.
FEATURES
source Location/Qualifiers
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/mol_type="genomic DNA"
/db_xref="taxon:9986"
/tissue_lib="rabbit genomic"
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/product="phospholamban"
/number=2
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524..682
/function="regulatory protein of sarcoplasmic reticulum
Ca-ATPase"
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/translation="MEKVQLTRSAIRRASTIEMPPQARQNLFNFCILICILL
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Best Local Similarity 94.3%; Pred. No. 5e-28;
Matches 150; Conservative 0; Mismatches 9; Indels 0; Gaps 0;
QY 1 ATGGGAAAAGTCCAATACCTCACTCGCTCAGCTATAAGAAGAGCCTCAACCAATTGAAATG 60
Db 524 ATGGGAAAAGTTCATATACCTCACTCGCTGCTATAGAAGAGCCTCAACCAATTGAAATG 583
QY 61 CCTCAACAGCAGCTCAAAAGCTACAGATCTATTATCAATTTCTGCTCATCTTAATA 120
Db 584 CCTCAACAGCAGCTCAAAAGCTCAACCACTTATCAATTTCTGCTCATCTTGA 643
QY 121 TGTCTCTTGTGATCTGTATCATCGTATGCTTCTCTGA 159
Db 644 TGTCTCTTGTGATCTGTATCATCGTATGCTTCTCTGA 682
RESULT 17
BD247907
LOCUS BD247907 159 bp DNA linear PAT 17-JUL-2003
DEFINITION Method for screening compounds.
ACCESSION BD247907
VERSION BD247907.1 GI:33057677
KEYWORDS JP 2002541859-A/9.
SOURCE Sus sp.
ORGANISM Sus sp.

QY	61	CCTCAACAGCAGCGTCAAAAGCTACAGAATCTATTATTAACAATTTCTGTCTCATCTTAATA	120
Db	61	CCTCAACAGCAGCGTCAAAAGCTACAGAATCTATTATTAACAATTTCTGTCTCATCTTAATA	120
QY	121	TGCTCTTGTCTGATCTGTATCATCTGATCGTCTCTCTGA	159
Db	121	TGCCTCTTGTCTGATTTGTCATCATCGTGATGCTTCTCTGA	159
RESULT 19			
AX040487			
LOCUS	AX040487	159 bp	DNA linear PAT 18-NOV-2000
DEFINITION	Sequence 9 from Patent WO0063426.		
ACCESSION	AX040487		
VERSION	AX040487.1	GI:11230276	
KEYWORDS	Sus sp.		
SOURCE	Sus sp.		
ORGANISM	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Laurasiatheria; Cetartiodactyla; Suina; Suidae; Sus.		
REFERENCE	1		
AUTHORS	Zwaal, R., Groenen, J. and Bogaert, T.		
TITLE	Compound screening methods		
JOURNAL	Patent: WO 0063426-A 9 26-OCT-2000; Devgen NV (BE)		
FEATURES	Location/Qualifiers		
source	1..159		
ORIGIN			
Query Match	89.9%;	Score 143;	DB 6; Length 159;
Best Local Similarity	93.7%;	Pred. No. 1.7e-27;	
Matches 149;	Conservative 0;	Mismatches 10;	Indels 0; Gaps 0;
QY	1	ATGGAGAAAGTCCAATACCTCACTCGCTCAGCTATAGAAGAGCGCTCAACCAATTGAAATG	60
Db	1	ATGGATAAAGTCCAAATACCTCACTCGCTCTGCTATTAGAAGAGCTTCAACCAATTGAAATG	60
QY	61	CCTCAACAGCAGCTCAAAAGCTACAGAATCTATTATCAATTTCTGCTCATCTTAATA	120
Db	61	CCTCAACAGCAGCTCAAAACCTTCAGAACCTTATTCATTTCTGCTCATCTTAATA	120
QY	121	TGCTCTTGTCTGATCTGTATCATCTGATGCTTCTCTGA	159
Db	121	TGCCTCTTGTGATTTGTCATCATCGTGATGCTTCTCTGA	159
RESULT 18			
AR302003			
LOCUS	AR302003	159 bp	DNA linear PAT 12-JUN-2003
DEFINITION	Sequence 9 from patent US 6540996.		
ACCESSION	AR302003		
VERSION	AR302003.1	GI:31689908	
KEYWORDS	Unknown.		
SOURCE	Unknown.		
ORGANISM	Unclassified.		
REFERENCE	1 (bases 1 to 159)		
AUTHORS	Zwaal, R., Groenen, J. and Bogaert, T.		
TITLE	Compound screening methods		
JOURNAL	Patent: US 6540996-A 9 01-APR-2003; Devgen NV; Ghent-Zwijnaarde; GBX;		
FEATURES	Location/Qualifiers		
source	1..159		
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Query Match	89.9%;	Score 143;	DB 6; Length 159;
Best Local Similarity	93.7%;	Pred. No. 1.7e-27;	
Matches 149;	Conservative 0;	Mismatches 10;	Indels 0; Gaps 0;
QY	1	ATGGAGAAAGTCCAATACCTCACTCGCTCAGCTATAGAAGAGCGCTCAACCAATTGAAATG	60
Db	1	ATGGATAAAGTCCAAATACCTCACTCGCTCTGCTATTAGAAGAGCTTCAACCAATTGAAATG	60
QY	1	ATGGAGAAAGTCCAATACCTCACTCGCTCAGCTATAGAAGAGCGCTCAACCAATTGAAATG	60
Db	1	ATGGATAAAGTCCAAATACCTCACTCGCTCTGCTATTAGAAGAGCTTCAACCAATTGAAATG	60

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Laurasiatheria; Cetartiodactyla; Suina; Suidae; Sus.	
1 (bases 1 to 159)	
Zwaal, R., Groenen, J. and Bogaert, T.	
Method for screening compounds	
Patent: JP 2002541859-A 9 10-DEC-2002;	
DEVGEN NV	
OS Sus sp. (pig)	
PN JP 2002541859-A/9	
PD 10-DEC-2002	
PR 14-APR-2000 JP 2000612503	60/129596 PR
PR 15-APR-1999 GB 9908670.4,15-APR-1999 US	
01-JUN-1999 GB 9912736.7	
PI RICHARD ZWAAL,JOSE GROENEN,THIERRY BOGAERT	
PC C12Q1/42,C12N15/09,C12Q1/02,C12N15/00	
CC Method for screening compounds	
KEYWORDS	
FH Key Location/Qualifiers	
FT source 1..159 /organism='Sus sp. (pig)'	
FT Location/Qualifiers	
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/organism='Sus sp.'	
/mol_type='genomic DNA'	
/db_xref='taxon:9826'	
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Query Match	89.9%; Score 143; DB 6; Length 159;
Best Local Similarity	93.7%; Pred. No. 1.7e-27;
Matches 149; Conservative 0; Mismatches 10; Indels 0; Gaps 0;	
QY	1 ATGGAGAAAGTCCAATACCTCACTCGCTCAGCTATAGAAGAGCGCTCAACCAATTGAAATG 60
Db	1 ATGGATAAAGTCCAAATACCTCACTCGCTCTGCTATTAGAAGAGCTTCAACCAATTGAAATG 60
QY	61 CCTCAACAGCAGCTCAAAAGCTACAGAATCTATTATCAATTTCTGCTCATCTTAATA 120
Db	61 CCTCAACAGCAGCTCAAAACCTTCAGAACCTTATTCATTTCTGCTCATCTTAATA 120
QY	121 TGCTCTTGTCTGATCTGTATCATCTGATGCTTCTCTGA 159
Db	121 TGCCTCTTGTGATTTGTCATCATCGTGATGCTTCTCTGA 159
RESULT 18	
AR302003	
LOCUS	AR302003 159 bp DNA linear PAT 12-JUN-2003
DEFINITION	Sequence 9 from patent US 6540996.
ACCESSION	AR302003
VERSION	AR302003.1 GI:31689908
KEYWORDS	Unknown.
SOURCE	Unknown.
ORGANISM	Unclassified.
REFERENCE	1 (bases 1 to 159)
AUTHORS	Zwaal, R., Groenen, J. and Bogaert, T.
TITLE	Compound screening methods
JOURNAL	Patent: US 6540996-A 9 01-APR-2003; Devgen NV; Ghent-Zwijnaarde; GBX;
FEATURES	Location/Qualifiers
source	1..159
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Query Match	89.9%; Score 143; DB 6; Length 159;
Best Local Similarity	93.7%; Pred. No. 1.7e-27;
Matches 149; Conservative 0; Mismatches 10; Indels 0; Gaps 0;	
QY	1 ATGGAGAAAGTCCAATACCTCACTCGCTCAGCTATAGAAGAGCGCTCAACCAATTGAAATG 60
Db	1 ATGGATAAAGTCCAAATACCTCACTCGCTCTGCTATTAGAAGAGCTTCAACCAATTGAAATG 60

JOURNAL Submitted (13-APR-1989) Eggermont J.A., Laboratorium Voor Fysiologie K.U. Leuven, Campus Gasthuisberg O/N, Herestraat 49, B-3000 Leuven, Belgium
COMMENT See <y00399> for canine phospholamban and <y00761> for rabbit phospholamban.
FEATURES Data kindly reviewed (12-OCT-1989) by Eggermont J. A.
source Location/Qualifiers
1..737
/organism="Sus scrofa"
/mol_type="mRNA"
/db_xref="taxon:9823"
/clone="PLB 7"
/tissue_type="smooth muscle"
/clone_lib="lambda gt11"
/dev_stage="2-day-old piglet"
173..331
/note="unnamed protein product; phospholamban (AA 1-52)"
CDS
1..737
/protein_id="CAA33171.1"
/db_xref="GI:2056"
/db_xref="GOA:P07473"
/db_xref="UniProt/Swiss-Prot:P07473"
/translation="MDKVQYLTRSAIRRASTIENPQQARQLNQLFINFCLILCLLL
ICIIVMLL"
misc_feature 716..721
/note="pot. polyA signal"
polyA_site 737
/note="polyA site"

ORIGIN
Query Match 89.9%; Score 143; DB 4; Length 737;
Best Local Similarity 93.7%; Pred. No. 1.4e-27;
Matches 149; Conservative 0; Mismatches 10; Indels 0; Gaps 0;
QY 1 ATGAGAAAGTCCAAATACCTCAGCTATAGAGAGGCTCAACCAATTGAAATG 60
DB 173 ATGATTAAGTCCAAATACCTCAGCTATAGAGAGGCTCAACCAATTGAAATG 232
QY 61 CCTCAACAGCAGCTCAAAAGCTACAGAACTATTATCAATTTCTCTCATCTTAATA 120
DB 233 CCTCAACAGCAGCTCAAAACCTTCAGAACTATTATCAATTTCTCTCATCTTAATA 292
QY 121 TGTCTCTTGTGATCTGTATCATCGTGATGCTTCTCTGA 159
DB 293 TGCCTCTTGTGATTTGTCATCATCGTGATGCTTCTCTGA 331
RESULT 21
LOCUS OCPHLM 2841 bp mRNA linear MAM 18-APR-2005
DEFINITION O. cuniculus mRNA for phospholamban.
ACCESSION Y00761
VERSION Y00761.1 GI:1661
KEYWORDS phospholamban.
SOURCE Oryctolagus cuniculus (rabbit)
ORGANISM Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Glires; Lagomorpha; Leporidae; Oryctolagus.
REFERENCE 1 (bases 1 to 2841)
AUTHORS Fujii, J., Lyttton, J., Tada, M. and MacLennan, D. H.
TITLE Rabbit cardiac and slow-twitch muscle express the same phospholamban gene
JOURNAL FEBS Lett. 227 (1), 51-55 (1988)
PUBMED 2962883
FEATURES Location/Qualifiers
1..2841
/organism="Oryctolagus cuniculus"
/mol_type="mRNA"
/db_xref="taxon:9986"
178..336
/codon_start=1
/product="phospholamban"

CDS
178..336
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/protein_id="CAA68730.1"
/db_xref="GI:1662"
/db_xref="GOA:P61015"
/db_xref="InterPro:IPR005984"
/db_xref="UniProt/Swiss-Prot:P61015"
/translation="MEKVQYLTRSAIRRASTIENPQQARQLNQLFINFCLILCLLL
ICIIVMLL"
ORIGIN
Query Match 89.9%; Score 143; DB 4; Length 2841;
Best Local Similarity 93.7%; Pred. No. 1.1e-27;
Matches 149; Conservative 0; Mismatches 10; Indels 0; Gaps 0;
QY 1 ATGAGAAAGTCCAAATACCTCAGCTATAGAGAGGCTCAACCAATTGAAATG 60
DB 178 ATGAGAAAGTCCAAATACCTCAGCTATAGAGAGGCTCAACCAATTGAAATG 237
QY 61 CCTCAACAGCAGCTCAAAAGCTACAGAACTATTATCAATTTCTCTCATCTTAATA 120
DB 238 CCTCAACAGCAGCTCAAAACCTTCAGAACTATTATCAATTTCTCTCATCTTAATA 297
QY 121 TGTCTCTTGTGATCTGTATCATCGTGATGCTTCTCTGA 159
DB 298 TGTCTCTTGTGATTTGTCATCATCGTGATGCTTCTCTGA 336
RESULT 22
LOCUS AY514751 314 bp DNA linear MAM 02-JUL-2004
DEFINITION Canis familiaris phospholamban (PLN) gene, complete cds.
ACCESSION AY514751
VERSION AY514751.1 GI:48476898
KEYWORDS Canis familiaris (dog)
ORGANISM Canis familiaris
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Laurasiatheria; Carnivora; Fissipedia; Canidae; Canis.
REFERENCE 1 (bases 1 to 314)
AUTHORS Housley, D. J. E., Ritzert, E. and Venta, P. J.
TITLE Comparative radiation hybrid map of canine chromosome 1 incorporating SNP and indel polymorphisms
JOURNAL Genomics 84 (2), 248-264 (2004)
REFERENCE 2 (bases 1 to 314)
AUTHORS Housley, D. J. E., Ritzert, E. and Venta, P. J.
TITLE Direct Submission
JOURNAL Submitted (29-DEC-2003) Small Animal Clinical Sciences and Microbiology and Molecular Genetics, Michigan State University, College of Veterinary Medicine, East Lansing, MI 48824-1314, USA
FEATURES Location/Qualifiers
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/organism="Canis familiaris"
/mol_type="genomic DNA"
/db_xref="taxon:9615"
/note="sequence information was obtained from a pool of ten breeds: German shepherd dog; Beagle; German shorthair pointer; Scottish terrier; Doberman pinscher; Greyhound; Siberian husky; Labrador retriever; Collie; Cocker spaniel; additional sequence was obtained from a single mixed breed dog of unknown origin"
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/codon_start=1

ORIGIN
Query Match 89.9%; Score 143; DB 4; Length 2841;
Best Local Similarity 93.7%; Pred. No. 1.1e-27;
Matches 149; Conservative 0; Mismatches 10; Indels 0; Gaps 0;
QY 1 ATGAGAAAGTCCAAATACCTCAGCTATAGAGAGGCTCAACCAATTGAAATG 60
DB 178 ATGAGAAAGTCCAAATACCTCAGCTATAGAGAGGCTCAACCAATTGAAATG 237
QY 61 CCTCAACAGCAGCTCAAAAGCTACAGAACTATTATCAATTTCTCTCATCTTAATA 120
DB 238 CCTCAACAGCAGCTCAAAACCTTCAGAACTATTATCAATTTCTCTCATCTTAATA 297
QY 121 TGTCTCTTGTGATCTGTATCATCGTGATGCTTCTCTGA 159
DB 298 TGTCTCTTGTGATTTGTCATCATCGTGATGCTTCTCTGA 336
RESULT 22
LOCUS AY514751 314 bp DNA linear MAM 02-JUL-2004
DEFINITION Canis familiaris phospholamban (PLN) gene, complete cds.
ACCESSION AY514751
VERSION AY514751.1 GI:48476898
KEYWORDS Canis familiaris (dog)
ORGANISM Canis familiaris
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Laurasiatheria; Carnivora; Fissipedia; Canidae; Canis.
REFERENCE 1 (bases 1 to 314)
AUTHORS Housley, D. J. E., Ritzert, E. and Venta, P. J.
TITLE Comparative radiation hybrid map of canine chromosome 1 incorporating SNP and indel polymorphisms
JOURNAL Genomics 84 (2), 248-264 (2004)
REFERENCE 2 (bases 1 to 314)
AUTHORS Housley, D. J. E., Ritzert, E. and Venta, P. J.
TITLE Direct Submission
JOURNAL Submitted (29-DEC-2003) Small Animal Clinical Sciences and Microbiology and Molecular Genetics, Michigan State University, College of Veterinary Medicine, East Lansing, MI 48824-1314, USA
FEATURES Location/Qualifiers
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ORIGIN
Query Match 89.9%; Score 143; DB 4; Length 2841;
Best Local Similarity 93.7%; Pred. No. 1.1e-27;
Matches 149; Conservative 0; Mismatches 10; Indels 0; Gaps 0;
QY 1 ATGAGAAAGTCCAAATACCTCAGCTATAGAGAGGCTCAACCAATTGAAATG 60
DB 178 ATGAGAAAGTCCAAATACCTCAGCTATAGAGAGGCTCAACCAATTGAAATG 237
QY 61 CCTCAACAGCAGCTCAAAAGCTACAGAACTATTATCAATTTCTCTCATCTTAATA 120
DB 238 CCTCAACAGCAGCTCAAAACCTTCAGAACTATTATCAATTTCTCTCATCTTAATA 297
QY 121 TGTCTCTTGTGATCTGTATCATCGTGATGCTTCTCTGA 159
DB 298 TGTCTCTTGTGATTTGTCATCATCGTGATGCTTCTCTGA 336
RESULT 22
LOCUS AY514751 314 bp DNA linear MAM 02-JUL-2004
DEFINITION Canis familiaris phospholamban (PLN) gene, complete cds.
ACCESSION AY514751
VERSION AY514751.1 GI:48476898
KEYWORDS Canis familiaris (dog)
ORGANISM Canis familiaris
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Laurasiatheria; Carnivora; Fissipedia; Canidae; Canis.
REFERENCE 1 (bases 1 to 314)
AUTHORS Housley, D. J. E., Ritzert, E. and Venta, P. J.
TITLE Comparative radiation hybrid map of canine chromosome 1 incorporating SNP and indel polymorphisms
JOURNAL Genomics 84 (2), 248-264 (2004)
REFERENCE 2 (bases 1 to 314)
AUTHORS Housley, D. J. E., Ritzert, E. and Venta, P. J.
TITLE Direct Submission
JOURNAL Submitted (29-DEC-2003) Small Animal Clinical Sciences and Microbiology and Molecular Genetics, Michigan State University, College of Veterinary Medicine, East Lansing, MI 48824-1314, USA
FEATURES Location/Qualifiers
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/organism="Canis familiaris"
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1..>314
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1..>314
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40..198
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Query Match 89.9%; Score 143; DB 4; Length 2841;
Best Local Similarity 93.7%; Pred. No. 1.1e-27;
Matches 149; Conservative 0; Mismatches 10; Indels 0; Gaps 0;
QY 1 ATGAGAAAGTCCAAATACCTCAGCTATAGAGAGGCTCAACCAATTGAAATG 60
DB 178 ATGAGAAAGTCCAAATACCTCAGCTATAGAGAGGCTCAACCAATTGAAATG 237
QY 61 CCTCAACAGCAGCTCAAAAGCTACAGAACTATTATCAATTTCTCTCATCTTAATA 120
DB 238 CCTCAACAGCAGCTCAAAACCTTCAGAACTATTATCAATTTCTCTCATCTTAATA 297
QY 121 TGTCTCTTGTGATCTGTATCATCGTGATGCTTCTCTGA 159
DB 298 TGTCTCTTGTGATTTGTCATCATCGTGATGCTTCTCTGA 336
RESULT 22
LOCUS AY514751 314 bp DNA linear MAM 02-JUL-2004
DEFINITION Canis familiaris phospholamban (PLN) gene, complete cds.
ACCESSION AY514751
VERSION AY514751.1 GI:48476898
KEYWORDS Canis familiaris (dog)
ORGANISM Canis familiaris
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Laurasiatheria; Carnivora; Fissipedia; Canidae; Canis.
REFERENCE 1 (bases 1 to 314)
AUTHORS Housley, D. J. E., Ritzert, E. and Venta, P. J.
TITLE Comparative radiation hybrid map of canine chromosome 1 incorporating SNP and indel polymorphisms
JOURNAL Genomics 84 (2), 248-264 (2004)
REFERENCE 2 (bases 1 to 314)
AUTHORS Housley, D. J. E., Ritzert, E. and Venta, P. J.
TITLE Direct Submission
JOURNAL Submitted (29-DEC-2003) Small Animal Clinical Sciences and Microbiology and Molecular Genetics, Michigan State University, College of Veterinary Medicine, East Lansing, MI 48824-1314, USA
FEATURES Location/Qualifiers
1..314
/organism="Canis familiaris"
/mol_type="genomic DNA"
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/note="sequence information was obtained from a pool of ten breeds: German shepherd dog; Beagle; German shorthair pointer; Scottish terrier; Doberman pinscher; Greyhound; Siberian husky; Labrador retriever; Collie; Cocker spaniel; additional sequence was obtained from a single mixed breed dog of unknown origin"
1..>314
/gene="PLN"
1..>314
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/gene="PLN"
40..198
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/gene="PLN"
/codon_start=1

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391..>669
/gene="PLN"

ORIGIN

Query Match 87.9%; Score 139.8; DB 4; Length 314;
Best Local Similarity 92.5%; Pred. No. 1.1e-26;
Matches 147; Conservative 0; Mismatches 12; Indels 0; Gaps 0;

QY 1 ATGGAGAAAGTCCATACCTCACTCGCTCAGCTATAGAGAGCGCTCAACCATTTGAAATG 60
DB 40 ATGGATAAAGTCCATACCTCACTCGCTCTGCTATTAGAAGAGCTTCAACCATTTGAAATG 99

QY 61 CCTCAACAGCAGCTCAAAAGCTACAGAACTATTATTATCAATTTCTGTCTCATCTTAATA 120
DB 100 CCTCAACAGCAGCTCAAAATCTTCAGAACCTATTATTATAAATTTCTGTCTCATTTAATA 159

QY 121 TGTCTCTTGTGATCTGTATCATCGTGATGCTTCTCTGA 159
DB 160 TGTCTCTTGTGATCTGTATCATCTGATGCTTCTCTGA 198

RESULT 23
AY576871S2
LOCUS
Canis familiaris phospholamban (PLN) gene, exon 2 and complete cds.
ACCESSION
AY576872
VERSION
AY576872.1 GI:48996075
SEGMENT
2 of 2
SOURCE
Canis familiaris (dog)
ORGANISM
Canis familiaris
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Laurasiatheria; Carnivora; Fissipedia; Canidae;
Canis.

REFERENCE
1 (bases 1 to 669)
Stabej, P., Leegwater, P.A., Stokhof, A.A. and van Oost, B.A.
Evaluation of the phospholamban gene in purebred dogs with dilated
cardiomyopathy
Unpublished
2 (bases 1 to 669)
Stabej, P., Leegwater, P.A. and van Oost, B.A.
Direct Submission
Submitted (19-MAR-2004) Clinical Sciences of Companion Animals,
Utrecht University, Yalelaan 8, Utrecht 3584CM, The Netherlands

FEATURES
Location/Qualifiers
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join(AY576871.1:201..283,131..231)
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131..>669
/gene="PLN"
/number=2
232..390
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ICIVMLL
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ORIGIN

Query Match 87.9%; Score 139.8; DB 4; Length 669;
Best Local Similarity 92.5%; Pred. No. 9.9e-27;
Matches 147; Conservative 0; Mismatches 12; Indels 0; Gaps 0;

QY 1 ATGGAGAAAGTCCATACCTCACTCGCTCAGCTATAGAGAGCGCTCAACCATTTGAAATG 60
DB 232 ATGGATAAAGTCCATACCTCACTCGCTCTGCTATTAGAAGAGCTTCAACCATTTGAAATG 291

QY 61 CCTCAACAGCAGCTCAAAAGCTACAGAACTATTATTATCAATTTCTGTCTCATCTTAATA 120
DB 232 CCTCAACAGCAGCTCAAAATCTTCAGAACCTATTATTATAAATTTCTGTCTCATTTAATA 351

QY 121 TGTCTCTTGTGATCTGTATCATCGTGATGCTTCTCTGA 159
DB 352 TGTCTCTTGTGATCTGTATCATCTGATGCTTCTCTGA 390

RESULT 24
DOGPHL
LOCUS
Canine cardiac phospholamban mRNA.
ACCESSION
M16012.1 GI:164043
VERSION
M16012.1
KEYWORDS
phospholamban.
SOURCE
Canis lupus (gray wolf)
ORGANISM
Canis lupus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Laurasiatheria; Carnivora; Fissipedia; Canidae;
Canis.

REFERENCE
1 (bases 1 to 832)
Fujii, J., Ueno, A., Kitano, K., Tanaka, S., Kadoma, M. and Tada, M.
Complete complementary DNA-derived amino acid sequence of canine
cardiac phospholamban
J. Clin. Invest. 79 (1), 301-304 (1987)
PUBMED
3793929
COMMENT
Original source text: Dog cDNA to mRNA.
FEATURES
Location/Qualifiers
source
1..832
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181..339
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ICIVMLL"

ORIGIN

Query Match 87.9%; Score 139.8; DB 4; Length 832;
Best Local Similarity 92.5%; Pred. No. 9.6e-27;
Matches 147; Conservative 0; Mismatches 12; Indels 0; Gaps 0;

QY 1 ATGGAGAAAGTCCATACCTCACTCGCTCAGCTATAGAGAGCGCTCAACCATTTGAAATG 60
DB 181 ATGGATAAAGTCCATACCTCACTCGCTCTGCTATTAGAAGAGCTTCAACCATTTGAAATG 240

QY 61 CCTCAACAGCAGCTCAAAAGCTACAGAACTATTATTATCAATTTCTGTCTCATCTTAATA 120
DB 241 CCTCAACAGCAGCTCAAAATCTTCAGAACCTATTATTATAAATTTCTGTCTCATTTAATA 300

QY 121 TGTCTCTTGTGATCTGTATCATCGTGATGCTTCTCTGA 159
DB 301 TGTCTCTTGTGATCTGTATCATCTGATGCTTCTCTGA 339

RESULT 25

DOGPBLA
LOCUS
DEFINITION
ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM
REFERENCE
AUTHORS
TITLE
JOURNAL
PUBMED
COMMENT
FEATURES
source
CDS

DOGPBLA
Dog cardiac phospholamban mRNA, complete cds.
M35393.1 GI:164045
phospholamban.
Canis sp.
Canis sp.
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Laurasiatheria; Carnivora; Fissipedia; Canidae;
Canis.
1 (bases 1 to 832)
Uyeda,A., Kitano,K., Fujii,J., Kadoma,M., Tada,M. and Tanaka,S.
Characterization of recombinant cDNA clones for canine cardiac
phospholamban
Nucleic Acids Symp. Ser. 17, 121-124 (1986)
3562256
Original source text: Dog heart, cDNA to mRNA, clone pPLB1.
Location/Qualifiers
1..832
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/db_xref="taxon:9616"
181..339
/note="cardiac phospholamban (EC 2.7.1.37)"
/codon_start=1
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/db_xref="GI:164046"
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ICIIIVMLL"

ORIGIN

Query Match 87.9%; Score 139.8; DB 4; Length 832;
Best Local Similarity 92.5%; Pred. No. 9.6e-27;
Matches 147; Conservative 0; Mismatches 12; Indels 0; Gaps 0;
Qy 1 ATGGAAGAAGTCCAAATACCTCCTCGCTCAGCTATAGAAGAGCCTCAACCATTTGAATG 60
Dy 181 ATGGAAGAAGTCCAAATACCTCCTCGCTCAGCTATAGAAGAGCCTCAACCATTTGAATG 240
Qy 61 CCTCAACAGCAGCTCAAAAGCTACAGAACTATTATCAATTTCTGCTCATCTTAATA 120
Dy 241 CCTCAACAGCAGCTCAAAATCTCAGAACCTATTATAAATTTCTGCTCATTTAATA 300
Qy 121 TGTCTCTTGTGATCTGTCATCATCGTCATGCTTCTCTGA 159
Dy 301 TGTCTCTTGTGATCTGTCATCATGTCATGCTTCTCTGA 339

RESULT 26

CFPHLX
LOCUS
DEFINITION
ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM
REFERENCE
AUTHORS
TITLE
JOURNAL
PUBMED
FEATURES
source
CDS

CFPHLX
Dog phospholamban mRNA, complete cds.
Y00399.1 M31636
Y00399.1 GI:911
phospholamban.
Canis familiaris (dog)
Canis familiaris
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Laurasiatheria; Carnivora; Fissipedia; Canidae;
Canis.
1 (bases 1 to 2614)
Uyeda,A., Kitano,K., Fujii,J., Kadoma,M., Tada,M. and Tanaka,S.
The cDNA sequence of the major phospholamban mRNA in canine cardiac
ventricular muscle
Nucleic Acids Res. 15 (16), 6738 (1987)
3628007
Location/Qualifiers
1..2614
/organism="Canis familiaris"
/mol_type="mRNA"
/db_xref="taxon:9615"
185..343

/note="unnamed protein product; phospholamban"
/codon_start=1
/protein_id="CAA68461.1"
/db_xref="GI:912"
/db_xref="GOA:P61012"
/db_xref="InterPro:IPR005984"
/db_xref="UniProt/SwissProt:P61012"
/translation="MDKVQLYTRSAIRRASTIEMPPQARQLNQLFINFCLILCLLL
ICIIIVMLL"

ORIGIN

Query Match 87.9%; Score 139.8; DB 4; Length 2614;
Best Local Similarity 92.5%; Pred. No. 8.1e-27;
Matches 147; Conservative 0; Mismatches 12; Indels 0; Gaps 0;
Qy 1 ATGGAAGAAGTCCAAATACCTCCTCGCTCAGCTATAGAAGAGCCTCAACCATTTGAATG 60
Dy 185 ATGGAAGAAGTCCAAATACCTCCTCGCTCAGCTATAGAAGAGCCTCAACCATTTGAATG 244
Qy 61 CCTCAACAGCAGCTCAAAAGCTACAGAACTATTATCAATTTCTGCTCATCTTAATA 120
Dy 245 CCTCAACAGCAGCTCAAAATCTCAGAACCTATTATAAATTTCTGCTCATTTAATA 304
Qy 121 TGTCTCTTGTGATCTGTCATCATCGTCATGCTTCTCTGA 159
Dy 305 TGTCTCTTGTGATCTGTCATCATGTCATGCTTCTCTGA 343

RESULT 27

AC013809
LOCUS
DEFINITION
ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM
REFERENCE
AUTHORS
TITLE
JOURNAL
REFERENCE
AUTHORS
TITLE
JOURNAL
COMMENT

AC013809
Homo sapiens clone RP11-21C18, LOW-PASS SEQUENCE SAMPLING.
AC013809
AC013809.4 GI:9123984
HTG; HTGS PHASE0.
Homo sapiens (human)
Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Homnidae; Homo.
1 (bases 1 to 179556)
Birren,B., Linton,L., Nusbaum,C. and Lander,E.
Homo sapiens, clone RP11-21C18
Unpublished
2 (bases 1 to 179556)
Birren,B., Linton,L., Nusbaum,C., Lander,E., Allen,N., Anderson,M.,
Baldwin,J., Barna,N., Beckerly,R., Boguslavsky,L., Boukhgalter,B.,
Brown,A., Castle,A., Colangelo,M., Collins,S., Collymore,A.,
Cooke,P., DeArelano,K., Dewar,K., Domino,M., Donegan,L., Doyle,M.,
Ferreira,P., Fitzhugh,W., Forrest,C., Funke,R., Gage,D.,
Galligan,J., Gardyna,S., Grant,G., Hagos,B., Heaford,A., Horton,L.,
Howland,J.C., Johnson,R., Jones,C., Kann,L., Karatas,A., Klein,J.,
Lehoczy,J., Lieu,C., Locke,K., Macdonald,P., Marquis,N.,
McEwan,P., McGurk,A., McKernan,K., McLaughlin,J., Meldrum,J.,
Morrow,J., Naylor,J., Norman,C.H., O'Connor,T., O'Donnell,P.,
Peterson,K., Pollara,V., Riley,R., Roy,A., Santos,R., Severy,P.,
Stange-Thomann,N., Stojanovic,N., Subramanian,A., Talamas,J.,
Tesfaye,S., Tirrell,A., Vassiliev,H., Vo,A., Wheeler,J., Wu,X.,
Wyman,D., Ye,W.J., Zimmer,A. and Zody,M.
Direct Submission
Submitted (15-NOV-1999) Whitehead Institute/MIT Center for Genome
Research, 320 Charles Street, Cambridge, MA 02141, USA
On Jul 13, 2000 this sequence version replaced gi:7107985.
All repeats were identified using RepeatMasker:
Smit, A.F.A. & Green, P. (1996-1997)
http://ftp.genome.washington.edu/RM/RepeatMasker.html
----- Genome Center
Center: Whitehead Institute/ MIT Center for Genome Research
Center code: WIBR
Web site: http://www-seq.wi.mit.edu
Contact: sequence_submissions@genome.wi.mit.edu
----- Project Information
Center project name: L3976

Center clone name: 21_C_18

* NOTE: This record contains 191 individual
 * sequencing reads that have not been assembled into
 * contigs. Runs of N are used to separate the reads
 * and the order in which they appear is completely
 * arbitrary. Low-pass sequence sampling is useful for
 * identifying clones that may be gene-rich and allows
 * overlap relationships among clones to be deduced.
 * However, it should not be assumed that this clone
 * will be sequenced to completion. In the event that
 * the record is updated, the accession number will
 * be preserved.

1	780:	contig of 780 bp in length
781	880:	gap of 100 bp
881	1631:	contig of 751 bp in length
1632	1731:	gap of 100 bp
1732	2490:	contig of 759 bp in length
2491	2590:	gap of 100 bp
2591	3363:	contig of 773 bp in length
3364	3463:	gap of 100 bp
3464	4235:	contig of 772 bp in length
4236	4335:	gap of 100 bp
4336	5117:	contig of 782 bp in length
5118	5217:	gap of 100 bp
5218	6006:	contig of 789 bp in length
6007	6106:	gap of 100 bp
6107	6869:	contig of 763 bp in length
6870	6969:	gap of 100 bp
6970	7733:	contig of 764 bp in length
7734	7833:	gap of 100 bp
7834	8607:	contig of 774 bp in length
8608	8707:	gap of 100 bp
8708	9479:	contig of 772 bp in length
9480	9579:	gap of 100 bp
9580	10344:	contig of 765 bp in length
10345	10444:	gap of 100 bp
10445	11212:	contig of 768 bp in length
11213	11312:	gap of 100 bp
11313	12056:	contig of 754 bp in length
12067	12166:	gap of 100 bp
12167	12972:	contig of 806 bp in length
12973	13072:	gap of 100 bp
13073	13842:	contig of 770 bp in length
13843	13942:	gap of 100 bp
13943	14708:	contig of 766 bp in length
14709	14808:	gap of 100 bp
14809	15579:	contig of 771 bp in length
15580	15679:	gap of 100 bp
15680	16450:	contig of 771 bp in length
16451	16550:	gap of 100 bp
16551	17324:	contig of 774 bp in length
17325	17424:	gap of 100 bp
17425	18199:	contig of 775 bp in length
18200	18299:	gap of 100 bp
18300	19041:	contig of 742 bp in length
19042	19141:	gap of 100 bp
19142	19940:	contig of 799 bp in length
19941	20040:	gap of 100 bp
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20793	20892:	gap of 100 bp
20893	21652:	contig of 760 bp in length
21653	21752:	gap of 100 bp
21753	22531:	contig of 779 bp in length
22532	22631:	gap of 100 bp
22632	23404:	contig of 773 bp in length
23405	23504:	gap of 100 bp
23505	24283:	contig of 779 bp in length
24284	24383:	gap of 100 bp
24384	25152:	contig of 769 bp in length
25153	25252:	gap of 100 bp
25253	26020:	contig of 768 bp in length
26021	26120:	gap of 100 bp
26121	26894:	contig of 774 bp in length
26895	27757:	gap of 100 bp
27758	28638:	contig of 781 bp in length
28639	28738:	gap of 100 bp
28739	29512:	contig of 774 bp in length
29513	29612:	gap of 100 bp
29613	30394:	contig of 782 bp in length
30395	30494:	gap of 100 bp
30495	31270:	contig of 776 bp in length
31271	31370:	gap of 100 bp
31371	32140:	contig of 770 bp in length
32141	32240:	gap of 100 bp
32241	33008:	contig of 768 bp in length
33009	33108:	gap of 100 bp
33109	33891:	contig of 783 bp in length
33892	33991:	gap of 100 bp
33992	34774:	contig of 783 bp in length
34775	34874:	gap of 100 bp
34875	35638:	contig of 764 bp in length
35639	35738:	gap of 100 bp
35739	36511:	contig of 773 bp in length
36512	36611:	gap of 100 bp
36612	37381:	contig of 770 bp in length
37382	37481:	gap of 100 bp
37482	38270:	contig of 789 bp in length
38271	38370:	gap of 100 bp
38371	39151:	contig of 781 bp in length
39152	39251:	gap of 100 bp
39252	40022:	contig of 771 bp in length
40023	40122:	gap of 100 bp
40123	40894:	contig of 772 bp in length
40895	40994:	gap of 100 bp
40995	41765:	contig of 771 bp in length
41766	41865:	gap of 100 bp
41866	42619:	contig of 754 bp in length
42620	42719:	gap of 100 bp
42720	43503:	contig of 784 bp in length
43504	43603:	gap of 100 bp
43604	44367:	contig of 764 bp in length
44368	44467:	gap of 100 bp
44468	45241:	contig of 774 bp in length
45242	45341:	gap of 100 bp
453		

Contact: MGC help desk
Email: cgapbe@mail.nih.gov
Tissue Procurement: Dr. Jonathan Kuo, NIMH
cDNA Library Preparation: Michael Brownstein / Ted Usdin
Laboratory
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (ILNL)
DNA Sequencing by: Sequencing Group at the Stanford Human Genome
Center, Stanford University School of Medicine, Stanford, CA 94305
Web site: <http://www-shgc.stanford.edu>
Contact: (Dickson, Mark) mcd@paxil.stanford.edu
Dickson, M., Schmutz, J., Grimwood, J., Rodriguez, A., and Myers,
R. M.

Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LNL at: <http://image.llnl.gov>
 Series: IRAL Plate: 53 Row: g Column: 14
 This clone was selected for full length sequencing because it passed the following selection criteria: matched mRNA gi: 12963502.

Source

Qy	61	CCTCAACAAGCAGCTCAAAAAGCTACAGAATCTATTATTCATTTCTGTCTCATCTTAATA	120
Db	131941	CCTCAACAAGCAGCTCAAAAAGCTACAGAATCTATTATTCATTTCTGTCTCATCTTAATA	
Qy	121	TGTCCTTGCTGATCTGTATCATCGTGA	148
Db	132001	TGTCCTTGCTGACTGAATCACCGGGA	132028

gene

RESULT 28			
BC061097	BC061097	648 bp	mRNA linear ROD 30-JUN-2004
		Mus musculus phospholamban, mRNA	(cDNA clone MGC:74215
DEFINITION		IMAGE:6772294), complete cds.	

CDS

ACCESSION BC061097
IMAGE:6772294, complete cds.
VERSION BC061097.1 GI:38173946
KEYWORDS MGC.
SOURCE Mus musculus (house mouse)

SOURCE Mus musculus (house mouse)

SOURCE	ORGANISM
Mus musculus (house mouse)	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi; Muridae; Muridae; Murinae; Mus.
Mus musculus	

SECRET

REFERENCE
AUTHORS
Sciurognathi; Muroidae; Muridae; Mus.
1 (bases 1 to 648)
Straussberg, R.L., Feingold, E.A., Grouse, L.H., Dorcas, J.C.

ORIGIN

	IC1IVMLL ^a	
Query Match	80.9%;	Score 128.6; DB 9; Length 648;
Best Local Similarity	88.1%;	Pred. No. 9.4e-24;
Matches 140; Conservative	0;	Mismatches 19; Indels 0; Gaps 0;
QY	1	ATGGAGAAAGTCCTCACTCCCTCAGCTATAGAAGAGCCTCAACCAATTGAAATG 60
Db	211	ATGAAAAGTGAATACCTCACTCCCTCGGTATCAGGAGAGCCTCCCACTATTGAAATG 270

1 ATGGAGAAAGTCCAATACTCACTCGCTCACTATAAGAGAGCGCTCAACCATTTGAAATG 60
 |||||
 211 ATGGAAAAGTGCATACTCACTCGCTCGCTATCAGGAGAGCTCCACTATTGCAATG 270
 |||||

20	61	CCTCAACAGACGCTCAAAGCTTACAGAAATCTATTTATCAATTTCTGTCATCTTAATA	120
20b	271	CCTCAGCAGCAGCTCAGAAATCTCCAGAACCTATTTATCAATTTGCGCTCATCTTGATA	330
20	121	TGTCCTCTGCTGATCTGTATATCATCGGTGCTCTCTGA	159
20b	331	TGTCCTGCTGATCTTGCCATCATTTGTGATGCTTCTGTGA	369

RESULT 29

[illegible]REMARK NIH-MGC Project URL: <http://mgc.ncbi.nlm.nih.gov> USA

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;

REFERENCE	Sciuognathi; Muridae; Murinae; Mus.
AUTHORS	1 (bases 1 to 940)
TITLE	Ganim,J.R., Luo,W., Ponniah,S., Grupp,I., Kim,H.W., Ferguson,D.G., Kadambi,V., Neumann,J.C., Doetschman,T. and Kranias,E.G. Mouse phospholamban gene expression during development in vivo and in vitro
JOURNAL	Circ. Res. 71 (5), 1021-1030 (1992)
PUBMED	1394867
REMARK	GenBank staff at the National Library of Medicine created this entry [NCBI gbbseq 116999] from the original journal article.
FEATURES	Location/Qualifiers
source	1. .940
	/organism="Mus sp."
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	/db_xref="taxon:10095"
gene	1. .940
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CDS	181. .339
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	/product="phospholamban"
	/protein_id="AAB23706.1"
	/db_xref="GI:257746"
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ORIGIN	
Query Match	80.9%; Score 128.6; DB 9; Length 940;
Best Local Similarity	88.1%; Pred. No. 8.9e-24;
Matches 140; Conservative	0; Mismatches 19; Indels 0; Gaps 0;
QY	1 ATGGAGAAGTCAATACCTCTCCTCAGCTATGAAGAGCCCTCAACCATTTGAATG 60
Db	181 ATGGAAAAAGTGAATACCTCTCCTCGGCTATCAGGAGCCCTCCATTTGAATG 240
QY	61 CCTCAACAAGCAGTCAAAAGCTACAGAACTATTTATCAATTTCTCTCATCTTAATA 120
Db	241 CCTCAGCAGCAGTCAAGATCTCCAGAACCTATTTATCAATTTCTGCTCATCTTGATA 300
QY	121 TGTCTCTTGCTGATCTGTATCATCGTGATGCTCTCTGA 159
Db	301 TGTCTGCTGCTGATCTGTCATCATTTGTGATGCTCTCTGTA 339
RESULT 30	
AC153524	AC153524 167574 bp DNA linear ROD 26-JAN-2005
LOCUS	Mus musculus 10 BAC RP23-349H12 (Roswell Park Cancer Institute (C57BL/6J Female) Mouse BAC Library) complete sequence.
DEFINITION	AC153524 AC099716
ACCESSION	AC153524.3 GI:58197576
VERSION	HTG.
KEYWORDS	Mus musculus (house mouse)
SOURCE	Mus musculus
ORGANISM	Eukaryota; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE	1 (bases 1 to 167574)
AUTHORS	Muzny,D., Adams,C., Agbai II,O., Allen,C., Alsbrooks,S., Archer,P., Arredondo,H., Bandaranaike,D., Bangura,L., Beltran,B., Beltran,R., Beraducci,A., Biswal,K., Blyth,P., Bonham,H., Buhay,C., Burch,P., Cadoree,I., Canada,A., Cardenas,V., Carter,K., Cavazos,I., Chacko,J., Chahrouh,M., Chavez,D., Chen,A., Chen,G., Chen,R., Cheng,M.-T., Chu,J., Clerc,K., Cockrell,R., Coyle,M., Cree,A., Curry,S., Dai,W., Davila,M.L., Davis,C., Davy-Carroll,L., De Anda,C., Delgado,O., Denson,S., Deramo,C., Ding,Y., Dinh,H., Donlin,J., McCauley,S., Dugan-Rocha,S., Dunn,A., Durbin,K., Dziuda,D., Egan,A., Escotto,M., Espinosa,V., Eugene,C., Fa,M., Fernandez,S., Fernando,P., Flagg,N., Forbes,L., Foster,P., Fowler,G., Fu,Q., Fuh,E., Garcia,A., Garcia,R., Garner,T., Gasikin,C., Genay,M., Guevara,W., Holder,M., Haaland,W., Haerberlen,K., Gonzalez-Garay,M., Hall,B., Hamid,H., Hamilton,K., Harbes,B., Harris,R., Havlak,P.,

Hawes, A., Hawkins, E., Hayes, S., Hemphill, L., Hernandez, J., Hines, S., Hitchens, M., Hodgson, A., Hogue, M., Hollins, B., Howell, L. T., Hulyk, S., Hume, J., Imo, K., Jackson, A., Jackson, L., Jacob, L., Jiang, H., Johnson, B., Johnson, R., Kalafus, K., Kelly, S., Keys, T., Khan, Z., King, L., Kovar, C., Kowis, A., Kowis, C., Lara, F., Leal, S., Lee, K., Lee, S., LeGall, F. I., Lemon, S., Lewis, L., Li, B., Li, Y., Li, Z., Linnell, M., Liu, W., Liu, Y.-S., Liu, Y., Liyanage, D., London, P., Lopez, J., Lorenuhewa, L., Lozado, R., Luk, T., Madu, R., Maheshwari, M., Mahoney, C., Malloy, K., Mansouri, D., Martinez, E., McClelland, H., McPherson, J., Mercadao, C., Metzker, M., Milosavljevic, A., Minja, E., Morgan, M., Morris, S., Munidasa, M., Murray, D., Nazarith, L., Ngo, D., Nguyen, N., Norwig-Eastaugh, E., Nott, A., Nwaokemeleh, O., Obregon, M., Ochi-Okorie, C., Odeh, E., Okwuonu, G., Okwuonu, K., Parker, D., Pasternak, S., Patel, B., Patel, V., Paul, H., Perez, A., Perez, L., Petrosino, J., Pham, T., Primus, E., Pu, L.-L., Puazo, M., Qin, X., Quinn, A., Quirzo, J., Rabata, D., Rachlin, E., Reigh, R., Ren, Y., Reuter, M., Richards, S., Trejos, Z., Umani, K., Vargo, C., Verduzco, D., Villasana, D., Virk, D., Volkov, A., Waldron, L., Walker, B., Wang, Q., Wang, S., Warren, J., Wei, X., Wheeler, S., Williams, G., Williams, R., Worley, K., Wright, R., Wu, J., Yakub, S., Yan, K., Yaun, Y., Yu, F., Zhang, J., Zhang, L., Zhang, Z., Zhou, J., Weinstock, G. and Gibbs, R.	
Direct Submission	
Unpublished	
2 (bases 1 to 167574)	
Worley, K.C.	
Direct Submission	
Submitted (14-DEC-2004)	Human Genome Sequencing Center, Baylor College of Medicine, One Baylor Plaza, Houston, TX 77030, USA
3 (bases 1 to 167574)	
Worley, K.C.	
Direct Submission	
Submitted (23-JAN-2005)	Human Genome Sequencing Center, Baylor College of Medicine, One Baylor Plaza, Houston, TX 77030, USA
4 (bases 1 to 167574)	
Worley, K.C.	
Direct Submission	
Submitted (26-JAN-2005)	Human Genome Sequencing Center, Baylor College of Medicine, One Baylor Plaza, Houston, TX 77030, USA
On Jan 26, 2005 this sequence version replaced gi:58037648.	
Sequencing is completed to a minimum standard of double strand coverage with a minimum of 2 clones and 2 reads with no ambiguities or 2 chemistries with a minimum of 2 clones and 3 reads with no ambiguities. If the sequence quality does not meet this standard, it will be indicated in the annotation.	
The repeat regions shown were identified using RepeatMasker by Adrian Smit.	
Sequence similarities were identified using Powerblast by Jinghui Zhang.	
Exon/Intron boundaries of identified genes were chosen if there were canonical splice junctions that maintained sequence continuity across the splice junctions.	
Location/Qualifiers	
1. .167574	
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/db_xref="taxon:10090"	
/chromosome="10"	
/clone="RP23-349H12"	
1. .32853	
/note="overlaps bases 134458. .167310 of clone AC105169"	
/function="clone overlap"	
55. .235	
/rpt_family="(TC)n"	
261. .366	
/rpt_family="MTE"	
misc_feature	
repeat_region	
repeat_region	

Qy 1 ATGGAGAAAGTCCATACCTCAGTCTCAGCTATAGAGAGAGCTCAACCATTTGAATG 60
Db 127 ATGGAAAAGTGCATACCTCAGTCTCGGCTATCAGAGAGCTCCACTATTGAAATG 186
Qy 61 CCTCAACAGCAGCTCAAAAAGCTACAGAAATCTATTATCAATTTCTGTCTCATCTTAATA 120
Db 187 CCTCAGCAGCAGCTCAGAAATCTCCAGAACCTATTATCAATTTCTGCTCATCTTGATA 246
Qy 121 TGTCTCTTGTGATCTGATCATCTGATGATGCTTCTCTGA 159
Db 247 TGTCTGCTGATCTGATCATCTGATGATGCTTCTGTGA 285

RESULT 32
AC100317
LOCUS Mus musculus clone RP23-124E8, LOW-PASS SEQUENCE SAMPLING.
DEFINITION AC100317
ACCESSION AC100317.1 GI:17047683
KEYWORDS HTG; HTGS_PHASE0.
SOURCE Mus musculus (house mouse)
ORGANISM Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;
Sciurognathi; Muridae; Murinae; Mus.
REFERENCE 1 (bases 1 to 79895)
AUTHORS Birren,B., Linton,L., Nusbaum,C. and Lander,B.
TITLE Mus musculus, clone RP23-124E8
JOURNAL Unpublished
REFERENCE 2 (bases 1 to 79895)
AUTHORS Birren,B., Linton,L., Nusbaum,C., Lander,B., Ali,A., Allen,N.,
Anderson,S., Barna,N., Bastien,V., Boguslavskiy,L., Boukhaltier,B.,
Brown,A., Camarata,J., Campopiano,A., Chang,J., Chazaro,B.,
Choepel,Y., Collangelo,M., Collins,S., Collymore,A., Cook,A.,
Cooke,P., DeArelano,W., Dewar,K., Diaz,J.S., Dodge,S., Faro,S.,
Ferreira,P., Fitzhugh,W., Gage,D., Galagan,J., Gardyna,S.,
Ginde,S., Gord,S., Goyette,M., Graham,L., Grand-Pierre,N.,
Hagos,B., Heatford,A., Horton,L., Hulme,W., Iliev,I., Johnson,R.,
Jones,C., Kamat,A., Karatas,A., Kells,C., Lakocque,K.,
Lamazzares,R., Landers,T., Lehoczy,J., Levine,R., Liu,G.,
Maclean,C., Macdonald,P., Major,J., Marquis,N., Matthews,C.,
McCarthy,M., McEwan,P., McKernan,K., McPheeters,R., Meldrum,J.,
Meneus,L., Mihova,T., Mlenga,V., Murphy,T., Naylor,J., O'Neil,D.,
Oliver,J., Peterson,K., Phunkhang,P., Pierre,N., Pollara,V.,
Raymond,C., Retta,R., Rieback,M., Riley,R., Rise,C., Rogov,P.,
Roman,J., Rosetti,M., Roy,A., Santos,R., Schauer,S., Schupback,R.,
Seaman,S., Severy,P., Spencer,B., Stange-Thomann,N., Stojanovic,N.,
Strauss,N., Subramanian,A., Talamas,J., Tesfaye,S., Theodore,J.,
Topham,K., Travers,M., Travis,N., Trigilio,J., Vassiliev,H.,
Viel,R., Vo,A., Wilson,B., Wu,X., Wyman,D., Ye,W.J., Young,G.,
Zainoun,J., Zembek,L., Zimmer,A. and Zody,M.
Direct Submission
Submitted (22-NOV-2001) Whitehead Institute/MIT Center for Genome
Research, 320 Charles Street, Cambridge, MA 02141, USA
All repeats were identified using RepeatMasker:
Smit, A.F.A. & Green, P. (1996-1997)
<http://ftp.genome.washington.edu/RM/RepeatMasker.html>
----- Genome Center
Center: Whitehead Institute/ MIT Center for Genome Research
Center code: WIER
Web site: <http://www-seq.wi.mit.edu>
Contact: sequence_submissions@genome.wi.mit.edu
----- Project Information
Center project name: L15083
Center clone name: 124_E_8

* NOTE: This record contains 74 individual
* sequencing reads that have not been assembled into
* contigs. Runs of N are used to separate the reads
* and the order in which they appear is completely
* arbitrary. Low-pass sequence sampling is useful for
* identifying clones that may be gene-rich and allows

* overlap relationships among clones to be deduced.
* However, it should not be assumed that this clone
* will be sequenced to completion. In the event that
* the record is updated, the accession number will
* be preserved.
1 986: contig of 986 bp in length
987 1086: gap of 100 bp
1087 1937: contig of 851 bp in length
1938 2037: gap of 100 bp
2038 3001: contig of 964 bp in length
3002 3101: gap of 100 bp
3102 4053: contig of 952 bp in length
4054 4153: gap of 100 bp
4154 5121: contig of 968 bp in length
5122 6182: contig of 961 bp in length
6183 6282: gap of 100 bp
6283 7234: contig of 952 bp in length
7235 7334: gap of 100 bp
7335 8357: contig of 1023 bp in length
8358 8457: gap of 100 bp
8459 9564: contig of 1007 bp in length
9565 10584: contig of 1020 bp in length
10585 10684: gap of 100 bp
10685 11702: contig of 1018 bp in length
11703 11802: gap of 100 bp
11803 12769: contig of 967 bp in length
12770 12869: gap of 100 bp
12870 13335: contig of 966 bp in length
13336 13935: gap of 100 bp
13936 14945: gap of 100 bp
14946 15925: contig of 980 bp in length
15926 16025: gap of 100 bp
16026 17040: contig of 1015 bp in length
17041 17140: gap of 100 bp
17141 18160: contig of 1020 bp in length
18161 19228: contig of 968 bp in length
19229 19328: gap of 100 bp
19330 20334: contig of 1006 bp in length
20335 21352: contig of 918 bp in length
21353 22407: contig of 955 bp in length
22408 22507: gap of 100 bp
22508 23480: contig of 973 bp in length
23481 23580: gap of 100 bp
23581 24553: contig of 973 bp in length
24554 25633: contig of 980 bp in length
25634 25733: gap of 100 bp
25734 26747: contig of 1014 bp in length
26748 26847: gap of 100 bp
26848 27857: contig of 1010 bp in length
27858 27957: gap of 100 bp
27959 28963: contig of 1006 bp in length
28964 29063: gap of 100 bp
29064 30073: contig of 1010 bp in length
30074 30173: gap of 100 bp
30174 31122: contig of 949 bp in length
31123 31222: gap of 100 bp
31223 32192: contig of 970 bp in length
32193 32292: gap of 100 bp
32293 33178: contig of 886 bp in length
33179 33278: gap of 100 bp
33279 34290: contig of 1012 bp in length
34291 34390: gap of 100 bp
34391 35386: contig of 996 bp in length
35387 35486: gap of 100 bp
35487 36494: contig of 1008 bp in length
36495 36594: gap of 100 bp

*	37579:	contig of 985 bp in length
*	37580:	gap of 100 bp
*	37679:	gap of 100 bp
*	37680:	contig of 1013 bp in length
*	38692:	contig of 1013 bp in length
*	38693:	gap of 100 bp
*	38792:	gap of 100 bp
*	38797:	contig of 1005 bp in length
*	38798:	gap of 100 bp
*	38998:	contig of 100 bp
*	40757:	contig of 860 bp in length
*	40758:	contig of 860 bp in length
*	40857:	gap of 100 bp
*	40858:	gap of 100 bp
*	41873:	contig of 1016 bp in length
*	41874:	gap of 100 bp
*	41974:	contig of 957 bp in length
*	42930:	contig of 957 bp in length
*	42931:	gap of 100 bp
*	43031:	contig of 953 bp in length
*	43983:	contig of 953 bp in length
*	44083:	gap of 100 bp
*	44084:	contig of 933 bp in length
*	45017:	contig of 933 bp in length
*	45116:	gap of 100 bp
*	45117:	contig of 988 bp in length
*	46104:	contig of 988 bp in length
*	46105:	gap of 100 bp
*	46200:	gap of 100 bp
*	46201:	contig of 1016 bp in length
*	46202:	contig of 1016 bp in length
*	47221:	gap of 100 bp
*	47320:	gap of 100 bp
*	47321:	contig of 996 bp in length
*	48316:	contig of 996 bp in length
*	48317:	gap of 100 bp
*	48417:	contig of 1005 bp in length
*	49421:	contig of 1005 bp in length
*	49422:	gap of 100 bp
*	49423:	contig of 954 bp in length
*	50475:	contig of 954 bp in length
*	50575:	gap of 100 bp
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*	51527:	gap of 100 bp
*	51528:	contig of 937 bp in length
*	52563:	contig of 937 bp in length
*	52564:	gap of 100 bp
*	52664:	contig of 985 bp in length
*	53648:	contig of 985 bp in length
*	53749:	gap of 100 bp
*	54722:	contig of 974 bp in length
*	54723:	gap of 100 bp
*	54823:	contig of 1016 bp in length
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*	55939:	gap of 100 bp
*	56910:	contig of 972 bp in length
*	56911:	contig of 972 bp in length
*	57011:	gap of 100 bp
*	57967:	contig of 957 bp in length
*	57968:	gap of 100 bp
*	58067:	gap of 100 bp
*	58068:	contig of 1012 bp in length
*	59080:	contig of 1012 bp in length
*	59179:	gap of 100 bp
*	59180:	contig of 991 bp in length
*	60170:	contig of 991 bp in length
*	60270:	gap of 100 bp
*	60271:	contig of 1031 bp in length
*	61301:	contig of 1031 bp in length
*	61401:	gap of 100 bp
*	61402:	contig of 1060 bp in length
*	62461:	contig of 1060 bp in length
*	62462:	gap of 100 bp
*	62562:	contig of 972 bp in length
*	63534:	contig of 972 bp in length
*	63634:	gap of 100 bp
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*	64592:	gap of 100 bp
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*	65674:	contig of 982 bp in length
*	65773:	gap of 100 bp
*	66768:	contig of 995 bp in length
*	66769:	contig of 995 bp in length
*	66869:	gap of 100 bp
*	67821:	contig of 953 bp in length
*	67822:	contig of 953 bp in length
*	67921:	gap of 100 bp
*	68923:	contig of 1002 bp in length
*	68924:	contig of 1002 bp in length
*	70050:	contig of 1027 bp in length
*	70051:	gap of 100 bp
*	70151:	contig of 1015 bp in length
*	71165:	contig of 1015 bp in length
*	71265:	gap of 100 bp
*	71266:	contig of 970 bp in length
*	72235:	contig of 970 bp in length
*	72236:	gap of 100 bp
*	72336:	contig of 1025 bp in length
*	73360:	contig of 1025 bp in length
*	73361:	gap of 100 bp
*	73461:	contig of 954 bp in length
Query Match		
Best Local Similarity		
Matches 139; Conservative		
79.9%; Score 127; DB 14; Length 79895;		
87.4%; Pred. No. 1.3e-23;		
0; Mismatches 20; Indels 0;		

```

VERSION      S95849.1  GI:247934
KEYWORDS
SOURCE
ORGANISM      Rattus sp.
               Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
               Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;
               Sciurognathi; Muroidea; Muridae; Murinae; Rattus.
REFERENCE     1 (bases 1 to 386)
AUTHORS       Hwang,K.S. and Nadal-Ginard,B.
TITLE         Cloning phospholamban cDNA from rat aortic smooth muscle
JOURNAL       Adv. Exp. Med. Biol. 304, 387-395 (1991)
PUBMED        1725098
REMARK        GenBank staff at the National Library of Medicine created this
               entry [NCBI gibseq 95849] from the original journal article.
               This sequence comes from Fig.2.
FEATURES
source       1..386
              /organism="Rattus sp."
              /mol_type="mRNA"
              /db_xref="taxon:10118"
              /tissue_type="cardiac smooth muscle"
gene         1..386
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              /db_xref="GI:26986719"
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              ICIIIVMLL"
CDS          159..317
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              /codon_start=1
              /product="phospholamban"
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              /db_xref="GI:26986719"
              /translation="MEKVQLTRSAIRRASTIEMPPQARQLNLFINFLILICLLL
              ICIIIVMLL"
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Best Local Similarity 86.8%; Pred. No. 7.2e-23;
Matches 138; Conservative 0; Mismatches 21; Indels 0; Gaps 0;
QY      1  ATGGAGAAAGTCCAATACCTCCTCAGCTATAGAGAGCCCTCAACCATTTGAAATG 60
Db      159  ATGGAAAAAGTCCAATACCTTACTCGCTCGGTATCAGGAGAGCCCTCGACTATTGAAATG 218
QY      61  CCTCACAGACGCTCAAAAGCTACAGAACTCTATTATCAATTTCTGCTCATCTTAATA 120
Db      219  CCCGACGACGCGTCAGAACCTCCAGAACCTTTTATCAATTTCTGCTCATCTTGATA 278
QY      121  TGTCTCTTGTGATCTGTATCATCGTATCGTCTCTCTGA 159
Db      279  TGTCTGCTGTGATCTGCATCATTTGTGATGCTTCTGTGA 317

RESULT 35
RATPHOLA02      1786 bp  DNA  linear  ROD 27-APR-1993
LOCUS      Rat phospholamban gene exon 2, complete cds.
DEFINITION
ACCESSION      L03382
VERSION        L03382.1  GI:206134
KEYWORDS       phospholamban.
SEGMENT        2 of 2
SOURCE         Rattus norvegicus (Norway rat)
ORGANISM       Rattus norvegicus
               Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
               Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;
               Sciurognathi; Muroidea; Muridae; Murinae; Rattus.
REFERENCE     1 (bases 1 to 1786)
AUTHORS       Johns,D.C. and Feldman,A.M.
TITLE         Identification of a highly conserved region at the 5' flank of the
               phospholamban gene
JOURNAL       Biochem. Biophys. Res. Commun. 188 (2), 927-933 (1992)
PUBMED        1445334
REMARK        Original source text: Rattus norvegicus (strain Sprague-Dawley)
               male adult liver DNA.
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               /mol_type="genomic DNA"
               /strain="Sprague-Dawley"
               /db_xref="taxon:10116"
               /sex="male"
               /tissue_type="liver"
               /dev_stage="adult"
               /order(L03381.1:1566..1836,1..704)
               /number=1
               /number=2
               /number=2
               /codon_start=1
               /product="phospholamban"
               /protein_id="AAA41849.1"
               /db_xref="GI:206136"
               /translation="MEKVQLTRSAIRRASTIEMPPQARQLNLFINFLILICLLL
               ICIIIVMLL"
intron
exon
CDS

```

* are represented as runs of N. The order of the pieces
 * is believed to be correct as given, however the sizes
 * of the gaps between them are based on estimates that have
 * provided by the submittor.
 * This sequence will be replaced
 * by the finished sequence as soon as it is available and
 * the accession number will be preserved.
 * 1 223728: contig of 223728 bp in length.

FEATURES
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 1. 223728
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 /mol_type="genomic DNA"
 /db_xref="taxon:10116"
 /clone="CH230-147118"
 1. 995
 /note="wgs contig"
 complement(217014..217851)
 /note="clone boundary"
 clone end:T7
 site:ECORI
 end_sequence:RWBAJ57TJB"

misc_feature
 misc_feature

ORIGIN
 Query Match 78.9%; Score 125.4; DB 14; Length 223728;
 Best Local Similarity 86.8%; Pred. No. 2.9e-23;
 Matches 138; Conservative 0; Mismatches 21; Indels 0; Gaps 0;
 Qy 1 ATGAGAAAGTCCAAATACCTCCTCGCTATGAGAGAGCTCAACCATTTGAATG 60
 Db 82163 ATGAGAAAGTCCAAATACCTCCTCGCTATGAGAGAGCTCAACCATTTGAATG 82222
 Qy 61 CCTCAACAGCAGCTCAAAAGCTACAGAACTATTATCAATTTCTGTCATCTTAATA 120
 Db 82223 CCCAGCAAGCGCTCAGAACTCCAGAACCTCTTTATCAATTTCTGTCATCTTGATA 82282
 Qy 121 TGTCTCTTGTGATCTGTCATCATCGTCGATGCTCTCTGA 159
 Db 82283 TGTCTCTGTCGATCTGTCATCATCTGTCGATGCTCTCTGA 82321

RESULT 37
 AC128365/c
 LOCUS
 DEFINITION Rattus norvegicus clone CH230-46019, WORKING DRAFT SEQUENCES, 2
 unordered pieces.
 AC128365
 VERSION AC128365.5 GI:25007909
 KEYWORDS HTG: HTGS PHASE1; HTGS DRAFT; HTGS_FULLTOP.
 SOURCE Rattus norvegicus (Norway rat)
 ORGANISM Rattus norvegicus
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;
 Sciurognathi; Muridea; Muridae; Murinae; Rattus.
 1 (bases 1 to 231910)
 Muzny, D., Marie, Metzker, M., Lee, S., Adams, C., Alder, J.,
 Allen, C., Allen, H., Alsbrooks, S., Amin, A., Anguiano, D.,
 Anyalebechi, V., Ayodeji, A., Ayodeji, M., Baca, E., Baden, H.,
 Baldwin, D., Bandaranaike, D., Barber, M., Barnstead, M., Benahmed, P.,
 Biswal, K., Blair, J., Blankenburg, K., Blyth, P., Brown, M.,
 Bryant, N., Buhay, C., Burch, P., Burrell, K., Calderon, E.,
 Cardenas, V., Carter, K., Cavazos, I., Ceasar, H., Center, A.,
 Chacko, J., Chavez, D., Chen, G., Chen, R., Chen, Y., Chen, Z., Chu, J.,
 Cleveland, C., Cockrell, R., Cox, C., Coyle, M., Cree, A., D'Souza, L.,
 Davila, M. L., Davis, C., Davy-Carroll, L., De Anda, C., Dederich, D.,
 Delgado, O., Denson, S., Deramo, C., Ding, Y., Dinh, H., Divya, K.,
 Draper, H., Dugan-Rocha, S., Dunn, A., Durbin, K., Duval, B., Evans, K.,
 Egan, A., Escotto, M., Eugene, C., Evans, C., Falls, T., Fan, G.,
 Fernandez, S., Finley, M., Flagg, N., Forbes, L., Foster, M., Foster, P.,
 Frazer, C. M., Gabisi, A., Ganta, R., Garcia, A., Garner, T., Garza, M.,
 Gregegeorgis, E., Geer, K., Gill, R., Grady, M., Guerra, W.,
 Gunaratne, P., Haaland, W., Hamil, C., Hamilton, C., Hamilton, K.,
 Harvey, Y., Havlak, P., Hawes, A., Henderson, N., Hernandez, J.,
 Hernandez, R., Hines, S., Hladun, S. L., Hodgson, A., Hogue, M.,

Liu, J., Liu, W., Liu, Y., London, P., Longacre, S., Lopez, J.,
 Lorensuhs, L., Loulgeed, H., Lozano, R. J., Lu, X., Ma, J.,
 Maheshwari, M., Mahindartne, M., Mahmoud, M., Malloy, K., Mangum, A.,
 Mangum, B., Mapua, P., Martin, K., Martin, R., Martinez, E.,
 Mawhiney, S., McLeod, M. P., McNeill, T. Z., Meenen, E.,
 Milosavljevic, A., Miner, G., Minja, E., Montanayor, J., Moore, S.,
 Morgan, M., Morris, K., Morris, S., Munidasa, M., Murphy, M., Nair, L.,
 Nankervis, C., Neal, D., Newton, N., Nguyen, N., Norris, S.,
 Nwankwelu, O., Okwuonu, G., Olarnpungoon, A., Pal, S., Parks, K.,
 Pasternak, S., Paul, H., Perez, A., Perez, L., Pfankuch, C.,
 Plapper, F., Poindexter, A., Popovic, D., Primus, E., Pu, L.,
 Puazo, M., Quiroz, J., Rachlin, E., Reeves, K., Regier, M. A., Reigh, R.,
 Reilly, B., Reilly, J., Rojas, A., Rose, M., Richards, S., Riggs, F.,
 Rivers, C., Rodkey, T., Royle, E., Reuter, M., Richards, S., Riggs, F.,
 Sanders, W., Savary, G., Scherer, S., Scott, G., Shatsman, S., Shen, H.,
 Shetty, J., Shvartsbeyn, A., Sisson, I., Sitter, C. D., Smajls, D.,
 Sneed, A., Sodergren, E., Song, X.-Z., Sorelle, R., Sosa, J.,
 Steimle, M., Strong, R., Sutton, A., Svatek, A., Tabor, P., Taylor, C.,
 Taylor, T., Thomas, N., Thomas, S., Tingey, A., Trejos, Z., Usmani, K.,
 Valas, R., Vera, V., Villanana, D., Waldron, L., Walker, B., Wang, J.,
 Wang, Q., Wang, S., Warren, J., Warren, R., Wei, X., White, F.,
 Williams, G., Willson, R., Wlezyk, R., Wooden, H., Worley, K.,
 Wright, D., Wright, R., Wu, J., Yakub, S., Yen, J., Yoon, L., Yoon, V.,
 Yu, F., Zhang, J., Zhou, J., Zhou, X., Zhao, S., Dunn, D., von
 Niederhausern, A., Weiss, R., Smith, D. R., Holt, R. A., Smith, H. O.,
 Weinstein, G. and Gibbs, R. A.

Direct Submission
 Unpublished
 2 (bases 1 to 223728)
 Worley, K. C.

Direct Submission
 Submitted (23-OCT-2001) Human Genome Sequencing Center, Department
 of Molecular and Human Genetics, Baylor College of Medicine, One
 Baylor Plaza, Houston, TX 77030, USA
 3 (bases 1 to 223728)

Rat Genome Sequencing Consortium.
 Direct Submission
 Submitted (10-MAY-2003) Human Genome Sequencing Center, Department
 of Molecular and Human Genetics, Baylor College of Medicine, One
 Baylor Plaza, Houston, TX 77030, USA
 On May 10, 2003 this sequence version replaced gi:24942703.
 The sequence in this assembly is a combination of BAC based reads
 and whole genome shotgun sequencing reads assembled using Atlas
 (<http://www.hgsc.bcm.tmc.edu/projects/rat/>). Each contig described
 in the feature table below represents a scaffold in the Atlas
 assembly (a 'contig-scaffold'). Within each contig-scaffold,
 individual sequence contigs are ordered and oriented, and separated
 by sized gaps filled with Ns to the estimated size. The sequence
 may extend beyond the ends of the clone and there may be sequence
 contigs within a contig-scaffold that consist entirely of whole
 genome shotgun sequence reads. Both end sequences and whole genome
 shotgun sequence only contigs will be indicated in the feature
 table.

----- Genome Center
 Center: Baylor College of Medicine
 Center code: BCM
 Web site: <http://www.hgsc.bcm.tmc.edu/>
 Contact: hgsc-help@bcm.tmc.edu
 ----- Project Information
 Center project name: GFOK
 Center clone name: CH230-147118
 ----- Summary Statistics
 Assembly program: Atlas 3.0;
 Consensus quality: 210120 bases at least Q40
 Consensus quality: 212963 bases at least Q30
 Consensus quality: 214568 bases at least Q20
 Estimated insert size: 220584; sum-of-contigs estimation
 Quality coverage: 7x in Q20 bases; sum-of-contigs estimation

* NOTE: Estimated insert size may differ from sequence length
 * (see http://www.hgsc.bcm.tmc.edu/docs/Genbank_draft_data.html).
 * NOTE: This is a 'working draft' sequence. It currently
 * consists of 1 contigs. Gaps between the contigs

TITLE
 JOURNAL
 REFERENCE
 AUTHORS
 TITLE
 JOURNAL
 REFERENCE
 AUTHORS
 TITLE
 JOURNAL
 COMMENT

Hollins,B., Howells,S., Hulyk,S., Hume,J., Idlebird,D., Jackson,A., Jackson,L., Jacob,L., Jiang,H., Johnson,B., Johnson,R., Jolivet,A., Karpthy,S., Kelly,S., Khan,Z., King,L., Kovar,C., Lewis,C., Kraft,C.L., Lebow,H., Levan,J., Lewis,L., Li,Z., Liu,J., Liu,J., Liu,W., Liu,Y., London,P., Longacre,S., Lopez,J., Lorensheva,L., Loulseged,H., Lozado,R.J., Lu,X., Ma,J., Maheshwari,M., Mahindartne,M., Mahmoud,M., Malloy,K., Mangum,A., Mangum,B., Mapua,P., Martin,K., Martin,R., Martinez,E., Mawhiney,S., McLeod,M.P., McNeill,T.Z., Meenen,E., Milosavljevic,A., Miner,G., Minja,E., Montemayor,J., Moore,S., Morgan,M., Morris,K., Morris,S., Munidasa,M., Murphy,M., Nair,L., Nankervis,C., Neal,D., Newton,N., Nguyen,N., Norris,S., Nwaokelimeh,O., Okwuonu,G., Olarunpungoon,A., Pal,S., Parks,K., Pasternak,S., Paul,H., Perez,A., Perez,L., Pfankoch,C., Plopper,F., Poindexter,A., Popovic,D., Primus,E., Pu,L.-L., Puzo,M., Quiroz,J., Rachlin,E., Reeves,K., Regier,M.A., Reigh,R., Reilly,B., Reilly,M., Ren,Y., Reuter,M., Richards,S., Riggs,F., Rives,C., Rodkey,T., Rojas,A., Rose,M., Rose,R., Ruiz,S.J., Sanders,W., Savery,G., Scherer,S., Scott,G., Shatman,S., Shen,H., Shetty,J., Shvartsbeyn,A., Sigson,I., Sitter,C.D., Smajls,D., Sneed,A., Sodergren,E., Song,X.-Z., Sorelle,R., Sosa,J., Steimle,M., Strong,R., Sutton,A., Svatek,A., Tabor,P., Taylor,C., Taylor,T., Thomas,N., Thomas,S., Tingey,A., Trejos,Z., Uemami,K., Valas,R., Vera,V., Villaseana,D., Waldron,L., Walker,B., Wang,J., Wang,Q., Wang,S., Warren,J., Warren,R., Wei,X., White,F., Williams,G., Willson,R., Wleczek,R., Wooden,H., Worley,K., Wright,D., Wright,R., Wu,J., Yakub,S., Yen,J., Yoon,L., Yoon,V., Yu,F., Zhang,J., Zhou,J., Zhou,X., Zhao,S., Dunn,D., von Niederhausern,A., Weiss,R., Smith,D.R., Holt,R.A., Smith,H.O., Weinstock,G. and Gibbs,R.A.

Direct Submission
Unpublished
2 (bases 1 to 231910)
Worley,K.C.

Direct Submission
Submitted (19-JUL-2002) Human Genome Sequencing Center, Department of Molecular and Human Genetics, Baylor College of Medicine, One Baylor Plaza, Houston, TX 77030, USA
3 (bases 1 to 231910)
Rat Genome Sequencing Consortium.

Direct Submission
Submitted (15-NOV-2002) Human Genome Sequencing Center, Department of Molecular and Human Genetics, Baylor College of Medicine, One Baylor Plaza, Houston, TX 77030, USA
On Nov 15, 2002 this sequence version replaced gi:23265008.
The sequence in this assembly is a combination of BAC based reads and whole genome shotgun sequencing reads assembled using Atlas (http://www.hgsc.bcm.tmc.edu/projects/rat/). Each contig described in the feature table below represents a scaffold in the Atlas assembly (a 'contig-scaffold'). Within each contig-scaffold, individual sequence contigs are ordered and oriented, and separated by sized gaps filled with Ns to the estimated size. The sequence may extend beyond the ends of the clone and there may be sequence contigs within a contig-scaffold that consist entirely of whole genome shotgun sequence reads. Both end sequences and whole genome shotgun sequence only contigs will be indicated in the feature table.

----- Genome Center
Center: Baylor College of Medicine
Center code: BCM
Web site: http://www.hgsc.bcm.tmc.edu/
Contact: hgsc-help@bcm.tmc.edu
----- Project Information
Center project name: GZBY
Center clone name: CH230-46019
----- Summary Statistics
Assembly program: Phrap; version 0.990329
Consensus quality: 226527 bases at least Q40
Consensus quality: 227741 bases at least Q30
Consensus quality: 228571 bases at least Q20
Estimated insert size: 231459; sum-of-contigs estimation
Quality coverage: 10x in Q20 bases; sum-of-contigs estimation

* NOTE: Estimated insert size may differ from sequence length
* (see http://www.hgsc.bcm.tmc.edu/docs/Genbank_draft_data.html).
* NOTE: This is a 'working draft' sequence. It currently
* consists of 2 contigs. The true order of the pieces
* is not known and their order in this sequence record is
* arbitrary. Gaps between the contigs are represented as
* runs of N, but the exact sizes of the gaps are unknown.
* This record will be updated with the finished sequence
* as soon as it is available and the accession number will
* be preserved.

* 1 230788: contig of 230788 bp in length
* 230789 230888: gap of unknown length
* 230889 231910: contig of 1022 bp in length.

FEATURES
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end sequence:BH332000"
complement(224996..225875)
/note="clone boundary
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site:
end sequence:BH332001"
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clone_end:Sp6"
230789..230888
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misc_feature
misc_feature
misc_feature
misc_feature
gap

ORIGIN
Query Match 78.9%; Score 125.4; DB 14; Length 231910;
Best Local Similarity 86.8%; Pred. No. 2.9e-23;
Matches 138; Conservative 0; Mismatches 21; Indels 0; Gaps 0;
QY 1 ATGGAGAAAGTCCAATACCTCTCGCTCAGCTATTAAGAGAGCCTCAACCATTTGAATG 60
Db 57561 ATGGAGAAAGTCCAATACCTCTCGCTCAGCTATTAAGAGAGCCTCAACCATTTGAATG 57502
QY 61 CCTCAACAGCAGCTCAAAAGCTACAGATCTATTATCAATTTCTGTCTCATCTTAATA 120
Db 57501 CCCACAGACGCGCTCAGAACCTCCAGAACCTCTTTATCAATTTCTGTCTCATCTTGA 57442
QY 121 TGTCTCTTGTGATCTGTATCATCGTGTGCTTCTCTGA 159
Db 57441 TGTCTCTTGTGATCTGTATCATCGTGTGCTTCTCTGA 57403

RESULT 38
RNPFLAMB
LOCUS RNPFLAMB 701 bp mRNA linear ROD 18-APR-2005
DEFINITION R.norvegicus mRNA for phospholamban.
ACCESSION X71068
VERSION X71068.1 GI:313809
KEYWORDS phospholamban.
SOURCE Rattus norvegicus (Norway rat)
ORGANISM Rattus norvegicus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;
Sciurognathi; Muridae; Murinae; Rattus.
1
Shanahan,C.M., Weissberg,P.L. and Metcalfe,J.C.
AUTHORS Isolation of gene markers of differentiated and proliferating
TITLE vascular smooth muscle cells
JOURNAL Circ. Res. 73 (1), 193-204 (1993)

PUBMED 8508530
REFERENCE 2 (bases 1 to 701)
AUTHORS Shanahan, C.M.
TITLE Direct Submission
JOURNAL Submitted (26-FEB-1993) C.M. Shanahan, University of Cambridge,
Dept of Biochemistry, Tennis Court Road, Cambridge CB2 1QW, UK
FEATURES Location/Qualifiers
source 1..701
/organism="Rattus norvegicus"
/mol_type="mRNA"
/strain="Wistar"
/db_xref="taxon:10116"
/clone="2RB7"
/tissue_type="aorta smooth muscle"
/clone_lib="lambda-Zap"
/dev_stage="adult"
174..332
/codon_start=1
/product="phospholamban"
/protein_id="CAA50394.1"
/db_xref="GI:313810"
/db_xref="GOA:P61016"
/db_xref="InterPro:IPR005984"
/db_xref="UniProt/Swiss-Prot:P61016"
/translation="MEKQVYITRSALRRASTLEVPQQRQLQELFVNFCILICLLL
ICIIIVMLL"

CDS

polyA_signal
polyA_site
polyA_signal
polyA_site
misc_feature
polyA_signal
polyA_site
ORIGIN

Query Match 77.9%; Score 123.8; DB 9; Length 701;
Best Local Similarity 86.2%; Pred. No. 1.8e-22;
Matches 137; Conservative 0; Mismatches 22; Indels 0; Gaps 0;

Qy 1 ATGGAGAAAGTCCAAATACCTCACTCGCTCAAGTATAAGAGAGCTCAACCATTTGAATG 60
Db 174 ATGGAAAAGTCCAAATACCTTACTCGCTCGGTATTAGGAGAGCTCGACTTTGAATG 233
Qy 61 CCTCAACAGCAGCTCAAGAGCTACAGAACTATTATCAATTTCTCTCATCTTAATA 120
Db 234 CCCAGCAGCGGTCAAGACCTCCAGAACCTCTTTATCAATTTCTCTCATCTTGATA 293
Qy 121 TGTCTCTTGTCTGATCTCTATCATCGTCAATGCTCTCTGA 159
Db 294 TGTCTGCTGATATGATCATGTCATGTCCTCTGGA 332

RESULT 39

CHKPLB2
LOCUS Chicken cardiac phospholamban (plb) mRNA linear VRT 06-MAR-1995
DEFINITION
ACCESSION M59039
VERSION M59039.1 GI:212575
KEYWORDS phospholamban.
SOURCE Gallus gallus (chicken)
ORGANISM Gallus gallus

REFERENCE

AUTHORS Toyofuku, T. and Zak, R.
TITLE Characterization of cDNA and genomic sequences encoding a chicken phospholamban
JOURNAL J. Biol. Chem. 266 (9), 5375-5383 (1991)
PUBMED 1825996
COMMENT Original source text: Chicken (broiler breeders) 7-week old adult heart, cDNA to mRNA, clones CPL-1, and CPL-15].
FEATURES Location/Qualifiers
source 1..3312
/organism="Gallus gallus"
/mol_type="mRNA"
/strain="broiler breeder"
/db_xref="taxon:9031"
/clone="CPL-15"
/clone="CPL-6"

/clone="CPL-12"
/tissue_type="heart"
/dev_stage="7-week old adult"
/tissue_lib="ZAP cDNA library"
1..3312
/gene="plb"
246..404
/gene="plb"
/codon_start=1
/product="phospholamban"
/protein_id="AAAG2738.1"
/db_xref="GI:212576"
/translation="MEKQVYITRSALRRASTLEVPQQRQLQELFVNFCILICLLL
ICIIIVMLL"
571..576
/gene="plb"
604
/gene="plb"
966..971
/gene="plb"
987
/gene="plb"
3071..3312
/gene="plb"
/notes="putative VECTOR sequence Bacteriophage lambda
(J02459); putative"
3290..3295
/gene="plb"
3312
/gene="plb"
ORIGIN

Query Match 68.8%; Score 109.4; DB 5; Length 3312;
Best Local Similarity 80.5%; Pred. No. 9.5e-19;
Matches 128; Conservative 0; Mismatches 31; Indels 0; Gaps 0;

Qy 1 ATGGAGAAAGTCCAAATACCTCACTCGCTCAAGTATAAGAGAGCTCAACCATTTGAATG 60
Db 246 ATGGAGAAAGTCCAAATACATAACCCGCTCTGCTCTGAGGAGAGCTCAACTCTTAGGTC 305
Qy 61 CCTCAACAGCAGCTCAAAAGCTACAGAACTATTATCAATTTCTCTCATCTTAATA 120
Db 306 AACCCACAGCAGCCAAAGGCTCCAGGAGCTCTTGTGAATTTGCGCTGATCTTAATT 365
Qy 121 TGTCTCTTGTCTGATCTGTATCATCGTCAATGCTCTCTGA 159
Db 366 TGCCTCTTGTCTGATCTGTATCATGTCATGTCCTCTGA 404

RESULT 40

CHKPLB2
LOCUS Chicken phospholamban (plb) gene, exon 2.
DEFINITION
ACCESSION M59038
VERSION M59038.1 GI:212578
KEYWORDS phospholamban.
SEGMENT 2 of 2
SOURCE Gallus gallus (chicken)
ORGANISM Gallus gallus

REFERENCE

AUTHORS Toyofuku, T. and Zak, R.
TITLE Characterization of cDNA and genomic sequences encoding a chicken phospholamban
J. Biol. Chem. 266 (9), 5375-5383 (1991)
PUBMED 1825996
COMMENT Original source text: Chicken (White leghorn) adult liver DNA, clones GPL-1, and GPL-2.
FEATURES Location/Qualifiers
source 1..3423
/organism="Gallus gallus"

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/mol_type="genomic DNA"
/strain="White leghorn"
/sub_species="domesticus"
/db_xref="taxon:9031"
/clone="GPL-1"
/tissue_type="adult"
/dev_stage="adult"
/tissue_lib="pEMBL3 chicken genomic"
Join(M59037.1:1511..1803,1..3423)
/gene="plb"
Join(M59037.1:1621..1745,89..3423)
/gene="plb"
/product="phospholamban"
Join(M59037.1:1621..1745,89..951)
/gene="plb"
/product="phospholamban"
Join(M59037.1:1621..1745,89..567)
/gene="plb"
/product="phospholamban"
order(M59037.1:1746..1803,1..88)
/gene="plb"
89..3423
/gene="plb"
/number=2
89..3276
/gene="plb"
/number=2
89..951
/gene="plb"
/number=2
89..567
/gene="plb"
/number=2
209..367
/gene="plb"
/codon_start=1
/product="phospholamban"
/protein_id="AAA63167.1"
/db_xref="GI:212580"
/translations="MEKQVYIIRSLRRASLTLEVNFPQRQLQELFVNFCLILCLL
ICIIIVMLL"
polyA_signal 534..539
/gene="plb"
polyA_signal 930..935
/gene="plb"
polyA_signal 3254..3259
/gene="plb"

ORIGIN
Query Match 68.8%; Score 109.4; DB 5; Length 3423;
Best Local Similarity 80.5%; Pred. No. 9.5e-19;
Matches 128; Conservative 0; Mismatches 31; Indels 0; Gaps 0;

1 ATGAGAGAAGTCCAAATACCTCAGCTGCTACAGCTATAAGAGAGCCTCAACATTGAATG 60
|||||
209 ATGAGAGAAGTCCAAATACATACACCGCTCTGCTCTGAGGAGAGCCTCAACTCTTGAGGTC 268
|||||
61 CCTCAACAAGCAGCTCAAAAGCTACAGATCTATTATCAATTTCTGCTCATCTTAATA 120
|||||
269 AACCCACAAGCAGCCAAAGCTCCAGAGCTCTTGTGAATTTCTGCTGATCTTAATT 328
|||||
121 TGTCTCTGCTGACTGTATCATCGTATGATGCTTCTCTGA 159
|||||
329 TGCCTCTTGTGATCTGTATCATTTGTGATGCTCTCTGA 367
|||||

RESULT 41
ARI21629 AR121629 315 bp DNA linear PAT 16-MAY-2001
LOCUS Sequence 26 from patent US 6160088.
DEFINITION
```

```
ACCESSION ARI21629
VERSION AR121629.1 GI:14105205
KEYWORDS
SOURCE
ORGANISM
REFERENCE 1 (bases 1 to 315)
AUTHORS Rothman,J.E., Mayhew,M. and Hoe,M.H.
TITLE KDEL receptor inhibitors
JOURNAL Patent: US 6160088-A 26 12-DEC-2000;
FEATURES
source
location/Qualifiers
1..315
/molecule_type="unknown"
/mol_type="unassigned DNA"

ORIGIN
Query Match 52.2%; Score 83; DB 6; Length 315;
Best Local Similarity 100.0%; Pred. No. 1.4e-11;
Matches 83; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 74 GTCAAAAGCTACAGAATCTATTATCAATTTCTGCTCATCTTAATATGCTCTTGTCTGA 133
|||||
Db 98 GTCAAAAGCTACAGAATCTATTATCAATTTCTGCTCATCTTAATATGCTCTTGTCTGA 157
|||||
QY 134 TCTGTATCATCGTGATGCTTCTC 156
|||||
Db 158 TCTGTATCATCGTGATGCTTCTC 180
|||||

RESULT 42
CR926459/c
LOCUS
DEFINITION Zebrafish DNA sequence from clone CH211-260022 in linkage group 20,
complete sequence.
ACCESSION CR926459
VERSION CR926459.7 GI:60302549
KEYWORDS HTG.
SOURCE Danio rerio (zebrafish)
ORGANISM
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Actinopterygii; Neopterygii; Teleostei; Ostariophysi;
Cypriniformes; Cyprinidae; Danio.
1 (bases 1 to 132837)
Henderson,C.
Direct Submission
Submitted (25-FEB-2005) Wellcome Trust Sanger Institute, Hinxton,
Cambridgeshire, CB10 1SA, UK. E-mail enquiries:
zf1sh-help@sanger.ac.uk Clone requests: clonerequest@sanger.ac.uk
On Feb 26, 2005 this sequence version replaced gi:60098210.
----- Genome Center
Center: Wellcome Trust Sanger Institute
Center code: SC
Web site: http://www.sanger.ac.uk
Contact: zf1sh-help@sanger.ac.uk
-----
During sequence assembly data is compared from overlapping clones.
Where differences are found these are annotated as variations
together with a note of the overlapping clone name. Note that the
variation annotation may not be found in the sequence submission
corresponding to the overlapping clone, as we submit sequences with
only a small overlap as described above.
This sequence was finished as follows unless otherwise noted: all
regions were either double-stranded or sequenced with an alternate
chemistry or covered by high quality data (i.e., phred quality >=
30); an attempt was made to resolve all sequencing problems, such
as compressions and repeats; all regions were covered by at least
one plasmid subclone or more than one M13 subclone; and the
assembly was confirmed by restriction digest, except on the rare
occasion of the clone being a YAC.
The following abbreviations are used to associate primary accession
numbers given in the feature table with their source databases:
Emi, EMBL; Swi, SWISSPROT; Tr, TREMBL; Wp, WORMPEP; Information
on the WORMPEP database can be found at
```

http://www.sanger.ac.uk/Projects/C_elegans/wormpep Clone-derived Zebrafish pUC subclones occasionally display inconsistency over the length of mononucleotide A/T runs and conserved TA repeats. Where this is found the longest good quality representation will be submitted.

Repeat names beginning 'Dr' were identified by the Recon repeat discovery system (Zhirong Bao and Sean Eddy, submitted), and those beginning 'dr' were identified by Rick Waterman (Stephen Johnson lab, WashU). For further information see http://www.sanger.ac.uk/Projects/D_rerio/fishmask.shtml CH211-260022 is from a CHORI-211 BAC library

FEATURES

source
1. 132837
Location/Qualifiers
/organism="Danio rerio"
/mol_type="genomic DNA"
/db_xref="taxon:7955"
/clone="CH211-260022"
/clone_lib="CHORI-211"

ORIGIN

Query Match 46.7%; Score 74.2; DB 5; Length 132837;
Best Local Similarity 66.7%; Pred. No. 1.3e-09;
Matches 106; Conservative 0; Mismatches 53; Indels 0; Gaps 0;
QY 1 ATGAGAGAGTCCAAATACCTCACTCGCTCAGCTATAGAGAGCCTCAACCATTTGAATG 60
|||||
Db 6222 ATGGAGAGTGCAGCACATGACACGGCGGCCATTTCGGCGGCGTCCACCATGGAGTT 6163
QY 61 CCTCAACAGCAGCTCAAAAGCTACAGAAATCTATTTATCAATTTCTGTCTCATCTTAATA 120
|||||
Db 6162 CCCCAACAGGCCAAGCAGACATGACGAGAGCTCTTCGTCACATCTTCGCTCATCTCATC 6103
QY 121 TGTCTCTTGTGATCTGTATCATCGTGATGCTCTCTGA 159
|||||
Db 6102 TGCCTGCTGCTCATCATCATCATGTTGTTGCTAATGTGA 6064

RESULT 43

BX537355
LOCUS
DEFINITION
BX537355 Zebrafish DNA sequence from clone DKEY-18H6 in linkage group 20,
complete sequence.
BX537355
VERSION
BX537355.13 GI:41222933
KEYWORDS
HTG.

SOURCE

ORGANISM
Danio rerio (zebrafish)
Danio rerio
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Actinopterygii; Neopterygii; Teleostei; Ostariophysi;
Cypriniformes; Cyprinidae; Danio.
1 (bases 1 to 133901)
Direct Submission
Submitted (22-JAN-2004) Wellcome Trust Sanger Institute, Hinxton,
Cambridgeshire, CB10 1SA, UK. E-mail enquiries:
zfish-help@sanger.ac.uk Clone requests: clonerequest@sanger.ac.uk
On Jan 23, 2004 this sequence version replaced gi:41060381.

REFERENCE

AUTHORS
TITLE
JOURNAL

COMMENT

Center: Wellcome Trust Sanger Institute
Center code: SC
Web site: <http://www.sanger.ac.uk>
Contact: zfish-help@sanger.ac.uk

During sequence assembly data is compared from overlapping clones.
Where differences are found these are annotated as variations
together with a note of the overlapping clone name. Note that the
variation annotation may not be found in the sequence submission
corresponding to the overlapping clone, as we submit sequences with
only a small overlap as described above.
This sequence was finished as follows unless otherwise noted: all
regions were either double-stranded or sequenced with an alternate
chemistry or covered by high quality data (i.e., phred quality >=

30); an attempt was made to resolve all sequencing problems, such
as compressions and repeats; all regions were covered by at least
one plasmid subclone or more than one M13 subclone; and the
assembly was confirmed by restriction digest, except on the rare
occasion of the clone being a YAC.

The following abbreviations are used to associate primary accession
numbers given in the feature table with their source databases:
Em: EMBL; Sw: SWISSPROT; Tr: TREMBL; Wp: WORMPEP; Information
on the WORMPEP database can be found at
http://www.sanger.ac.uk/Projects/C_elegans/wormpep
Zebrafish pUC subclones occasionally display inconsistency over the
length of mononucleotide A/T runs and conserved TA repeats. Where
this is found the longest good quality representation will be
submitted.

Repeat names beginning 'Dr' were identified by the Recon repeat
discovery system (Zhirong Bao and Sean Eddy, submitted), and those
beginning 'dr' were identified by Rick Waterman (Stephen Johnson
lab, WashU). For further information see
http://www.sanger.ac.uk/Projects/D_rerio/fishmask.shtml DKEY-18H6
is from a Zebrafish BAC library

VECTOR: pIndigoBAC-5.

Location/Qualifiers
1. 133901
/organism="Danio rerio"
/mol_type="genomic DNA"
/db_xref="taxon:7955"
/clone="DKEY-18H6"
/clone_lib="DanioKey"

ORIGIN

Query Match 46.7%; Score 74.2; DB 5; Length 133901;
Best Local Similarity 66.7%; Pred. No. 1.3e-09;
Matches 106; Conservative 0; Mismatches 53; Indels 0; Gaps 0;
QY 1 ATGAGAGAGTCCAAATACCTCACTCGCTCAGCTATAGAGAGCCTCAACCATTTGAATG 60
|||||
Db 127680 ATGGAGAGTGCAGCACATGACACGGCGGCCATTTCGGCGGCGTCCACCATGGAGTT 127739
QY 61 CCTCAACAGCAGCTCAAAAGCTACAGAAATCTATTTATCAATTTCTGTCTCATCTTAATA 120
|||||
Db 127740 CCCCAACAGGCCAAGCAGACATGACGAGAGCTCTTCGTCACATCTTCGCTCATCTCATC 127799
QY 121 TGTCTCTTGTGATCTGTATCATCGTGATGCTCTCTGA 159
|||||
Db 127800 TGCCTGCTGCTCATCTACATCATGTTGTTGCTAATGTGA 127838

RESULT 44

BX276081
LOCUS
DEFINITION
BX276081 Zebrafish DNA sequence from clone CH211-270G19 in linkage group 10,
complete sequence.
BX276081
VERSION
BX276081.12 GI:47550483
KEYWORDS
HTG.

ACCESSION

ORGANISM

SOURCE

Danio rerio (zebrafish)
Danio rerio
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Actinopterygii; Neopterygii; Teleostei; Ostariophysi;
Cypriniformes; Cyprinidae; Danio.
1 (bases 1 to 130240)
Heath, P.
Direct Submission
Submitted (20-MAY-2004) Wellcome Trust Sanger Institute, Hinxton,
Cambridgeshire, CB10 1SA, UK. E-mail enquiries:
zfish-help@sanger.ac.uk Clone requests: clonerequest@sanger.ac.uk
On May 20, 2004 this sequence version replaced gi:46194142.

REFERENCE

AUTHORS

TITLE

JOURNAL

COMMENT

Center: Wellcome Trust Sanger Institute
Center code: SC
Web site: <http://www.sanger.ac.uk>
Contact: zfish-help@sanger.ac.uk

During sequence assembly data is compared from overlapping clones. Where differences are found these are annotated as variations together with a note of the overlapping clone name. Note that the variation annotation may not be found in the sequence submission corresponding to the overlapping clone, as we submit sequences with only a small overlap as described above.

This sequence was finished as follows unless otherwise noted: all regions were either double-stranded or sequenced with an alternate chemistry or covered by high quality data (i.e., phred quality >= 30); an attempt was made to resolve all sequencing problems, such as compressions and repeats; all regions were covered by at least one plasmid subclone or more than one M13 subclone; and the assembly was confirmed by restriction digest, except on the rare occasion of the clone being a YAC.

The following abbreviations are used to associate primary accession numbers given in the feature table with their source databases: Em; ENBL; Sw; SWISSPROT; Tr; TREMBL; Wp; WORMPEP; Information on the WORMPEP database can be found at http://www.sanger.ac.uk/projects/C_elegans/wormpep Clone-derived Zebrafish pUC subclones occasionally display inconsistency over the length of mononucleotide A/T runs and conserved TA repeats. Where this is found the longest good quality representation will be submitted.

Repeat names beginning 'Dr' were identified by the Recon repeat discovery system (Zhirong Bao and Sean Eddy, submitted), and those beginning 'drr' were identified by Rick Waterman (Stephen Johnson lab, WashU). For further information see http://www.sanger.ac.uk/projects/D_rerio/fishmask.shtml CH211-270G19 is from a CHORI-211 BAC library

VECTOR: pTARBAC2.1.

Location/Qualifiers

1. .130240

/organism="Danio rerio"

/mol_type="genomic DNA"

/db_xref="taxon:7955"

/clone="CH211-270G19"

/clone_lib="CHORI-211"

FEATURES

source

Query Match 44.7%; Score 71; DB 5; Length 130240;

Best Local Similarity 65.4%; Pred. No. 9.3e-09;

Matches 104; Conservative 0; Mismatches 55; Indels 0; Gaps 0;

QY 1 ATGAGAGAGTCAATACCTCCTCGTACGCTATGAGAGAGCCCTCAACATTTGAAATG 60

Db 92335 ATGAGAGGGGTGAGCATATGACGGCTCTGCGATCCGGAGAGCATCCACATCGAGGTG 92394

QY 61 CCTCAACAAGCAGCTCAAAAGCTACAGAACTCTATTTATCAATTTCTGCTCTCATTTAATA 120

Db 92395 AACCCGAGACCAACGCACTACAGGATCTCATCATCAACTTCTCCCTCATCTTAATC 92454

QY 121 TGCTCTTGTGATCTGATCTATCATCGTATCGTCTTCTGTA 159

Db 92455 TGCTCTGCTCATCTACATCATCTGCTTGTCTATGTGA 92493

RESULT 45

AC013809/c

LOCUS AC013809 179556 bp DNA linear HTG 13-JUL-2000

DEFINITION Homo sapiens clone RP11-21C18, LOW-PASS SEQUENCE SAMPLING.

ACCESSION AC013809

VERSION AC013809.4 GI:9123984

KEYWORDS HTG; HTGS PHASE0.

SOURCE Homo sapiens (human)

ORGANISM Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae; Homo.

REFERENCE 1 (bases 1 to 179556)

AUTHORS Birren,B., Linton,L., Nusbaum,C. and Lander,E.

TITLE Homo sapiens, clone RP11-21C18

JOURNAL Unpublished

REFERENCE 2 (bases 1 to 179556)

AUTHORS

Birren,B., Linton,L., Nusbaum,C., Lander,E., Allen,N., Anderson,M., Baldwin,J., Barna,N., Beckerly,R., Boguslavsky,L., Boukhgalter,B., Brown,A., Castle,A., Colangelo,M., Collins,S., Collamore,A., Cooke,P., Dearellano,K., Dewar,K., Domino,M., Doneilan,L., Doyle,M., Ferreira,P., FitzHugh,W., Forrest,C., Funke,R., Gage,D., Galagan,J., Gardyna,S., Grant,G., Hagos,B., Heaford,A., Horton,L., Howland,J.C., Johnson,R., Jones,C., Kann,L., Karatas,A., Klein,J., Lehoczy,J., Lieu,C., Locke,K., Macdonald,P., Marquis,N., McEwan,P., McGurk,A., McKernan,K., McLaughlin,J., Meldrum,J., Morrow,J., Naylor,J., Norman,C.H., O'Connor,T., O'Donnell,P., Peterson,K., Pollara,V., Rileigh,R., Roy,A., Santos,R., Severy,P., Stange-Thomann,N., Stojanovic,N., Subramanian,A., Talamas,J., Tesfaye,S., Tirrell,A., Vassiliev,H., Vo,A., Wheeler,J., Wu,X., Wyman,D., Ye,W.J., Zimmer,A. and Zody,M.

Direct Submission

Submitted (15-NOV-1999) Whitehead Institute/MIT Center for Genome Research, 320 Charles Street, Cambridge, MA 02141, USA

On Jul 13, 2000 this sequence version replaced gi:7107985.

All repeats were identified using RepeatMasker:

Smt, A.F.A. & Green, P. (1996-1997)

<http://ftp.genome.washington.edu/RM/RepeatMasker.html>

----- Genome Center

Center: Whitehead Institute/ MIT Center for Genome Research

Center code: WIBR

Web site: <http://www-seq.wi.mit.edu>

Contact: sequence_submissions@genome.wi.mit.edu

----- Project Information

Center project name: L3976

Center clone name: 21_C_18

* NOTE: This record contains 191 individual

* sequencing reads that have not been assembled into

* contigs. Runs of N are used to separate the reads

* and the order in which they appear is completely

* arbitrary. Low-pass sequence sampling is useful for

* identifying clones that may be gene-rich and allows

* overlap relationships among clones to be deduced.

* However, it should not be assumed that this clone

* will be sequenced to completion. In the event that

* the record is updated, the accession number will

* be preserved.

* 1

* 780: contig of 780 bp in length

* 781

* 880: gap of 100 bp

* 881

* 1631: contig of 751 bp in length

* 1632

* 1731: gap of 100 bp

* 1732

* 2490: contig of 759 bp in length

* 2491

* 2590: gap of 100 bp

* 2591

* 3363: contig of 773 bp in length

* 3364

* 3463: gap of 100 bp

* 3464

* 4235: contig of 772 bp in length

* 4236

* 4335: gap of 100 bp

* 4336

* 5117: contig of 782 bp in length

* 5118

* 5217: gap of 100 bp

* 5218

* 6006: contig of 789 bp in length

* 6007

* 6106: gap of 100 bp

* 6107

* 6869: contig of 763 bp in length

* 6870

* 6970: gap of 100 bp

* 6971

* 7733: contig of 764 bp in length

* 7734

* 7833: gap of 100 bp

* 7834

* 8607: contig of 774 bp in length

* 8608

* 8707: gap of 100 bp

* 8708

* 9479: contig of 772 bp in length

* 9480

* 9579: gap of 100 bp

* 9580

* 10344: contig of 765 bp in length

* 10345

* 10444: gap of 100 bp

* 10445

* 11212: contig of 768 bp in length

* 11213

* 11312: gap of 100 bp

* 11313

* 12066: contig of 754 bp in length

* 12067

* 12166: gap of 100 bp

* 12167

* 12972: contig of 806 bp in length

* 12973

* 13072: gap of 100 bp

* 13073

* 13842: contig of 770 bp in length

* 13843

* 13942: gap of 100 bp

JOURNAL Submitted (27-SEP-2000) DOE Joint Genome Institute, 2800 Mitchell Drive, Walnut Creek, CA 94598, USA

REFERENCE 4 (bases 1 to 134286)

AUTHORS DOE Joint Genome Institute and Stanford Human Genome Center.

TITLE Direct Submission

JOURNAL Submitted (03-OCT-2001) DOE Joint Genome Institute, 2800 Mitchell Drive, Walnut Creek, CA 94598, USA

COMMENT On Oct 3, 2001 this sequence version replaced gi:10312258.
Draft Sequence Produced by DOE Joint Genome Institute
www.jgi.doe.gov
Finishing Completed at Stanford Human Genome Center
www-shgc.stanford.edu
Quality: Phrap Quality >40 99.5% of Sequence;
Estimated Total Number of Errors is 0.6.

FEATURES
source Location/Qualifiers
1..134286
/organism="Homo sapiens"
/db_xref="taxon:9606"
/chromosome="5"
/clone="CTD-2203L19"

ORIGIN
Query Match 23.1%; Score 36.8; DB 8; Length 134286;
Best Local Similarity 58.0%; Pred. No. 11;
Matches 65; Conservative 0; Mismatches 47; Indels 0; Gaps 0;

QY 46 TCAACCATTTGAATGCTCAACAGCAGCTCAAAAGCTACAGAATCTATTATCAATTC 105
|||||
DB 40650 TCAACCTTTGATCGATTCTACATATAAGTGAACCGTACAGAAATTTTCATCTCTGTTTC 40709
|||||

QY 106 TGTCTCATCTTAATATGCTCTTGGCTGATCTGTATCATCGTATGCTTCTCT 157
|||||

DB 40710 TGGCTTTATTTCACTGAGCATATAATAGGCTCTCTAAATTCATCTGTTTTT 40761
|||||

RESULT 47

AC024589 170272 bp DNA linear PRI 15-AUG-2001

LOCUS Homo sapiens chromosome 5 clone RP11-42L13, complete sequence.

DEFINITION AC024589

ACCESSION AC024589.5 GI:15187245

VERSION

KEYWORDS HTG.

SOURCE Homo sapiens (human)

ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Homnidae; Homo.

REFERENCE 1 (bases 1 to 170272)

AUTHORS DOE Joint Genome Institute and Stanford Human Genome Center.

TITLE Direct Submission

JOURNAL Unpublished

REFERENCE 2 (bases 1 to 170272)

AUTHORS DOE Joint Genome Institute.

TITLE Direct Submission

JOURNAL Submitted (29-FEB-2000) Production Sequencing Facility, DOE Joint Genome Institute, 2800 Mitchell Drive, Walnut Creek, CA 94598, USA

REFERENCE 3 (bases 1 to 170272)

AUTHORS DOE Joint Genome Institute and Stanford Human Genome Center.

TITLE Direct Submission

JOURNAL Submitted (01-MAR-2001) DOE Joint Genome Institute, 2800 Mitchell Drive, Walnut Creek, CA 94598, USA

REFERENCE 4 (bases 1 to 170272)

AUTHORS DOE Joint Genome Institute and Stanford Human Genome Center.

TITLE Direct Submission

JOURNAL Submitted (15-AUG-2001) DOE Joint Genome Institute, 2800 Mitchell Drive, Walnut Creek, CA 94598, USA

COMMENT On Aug 15, 2001 this sequence version replaced gi:13173623.
Draft Sequence Produced by DOE Joint Genome Institute
www.jgi.doe.gov
Finishing Completed at Stanford Human Genome Center
www-shgc.stanford.edu
Quality: Phrap Quality >40 99.8% of Sequence;

Estimated Total Number of Errors is 0.2.

FEATURES
source Location/Qualifiers
1..170272
/organism="Homo sapiens"
/mol_type="genomic DNA"
/db_xref="taxon:9606"
/chromosome="5"
/clone="RP11-42L13"

ORIGIN
Query Match 23.1%; Score 36.8; DB 8; Length 170272;
Best Local Similarity 58.0%; Pred. No. 11;
Matches 65; Conservative 0; Mismatches 47; Indels 0; Gaps 0;

QY 46 TCAACCATTTGAATGCTCAACAGCAGCTCAAAAGCTACAGAATCTATTATCAATTC 105
|||||

DB 9253 TCAACCTTTGATCGATTCTACATATAAGTGAACCGTACAGAAATTTTCATCTCTGTTTC 9312
|||||

QY 106 TGTCTCATCTTAATATGCTCTTGGCTGATCTGTATCATCGTATGCTTCTCT 157
|||||

DB 9313 TGGCTTTATTTCACTGAGCATATAATAGGCTCTCTAAATTCATCTGTTTTT 9364
|||||

RESULT 48

AL590653 116103 bp DNA linear PRI 18-MAY-2005

LOCUS Human DNA sequence from clone RP11-142B3 on chromosome 1 Contains part of the gene for melanoma antigen recognized by T cells 2

DEFINITION Protein (MART2), complete sequence.

ACCESSION AL590653

VERSION AL590653.11 GI:17384115

KEYWORDS HTG; MART2; melanoma antigen; T cells 2 protein.

SOURCE Homo sapiens (human)

ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Homnidae; Homo.

REFERENCE 1 (bases 1 to 116103)

AUTHORS Harrison,E.

TITLE Direct Submission

JOURNAL Submitted (13-MAY-2005) Wellcome Trust Sanger Institute, Hinxton, Cambridgeshire, CB10 1SA, UK. E-mail enquiries: vegas@sanger.ac.uk

COMMENT On Dec 5, 2001 this sequence version replaced gi:17127779.
The following abbreviations are used to associate primary accession numbers given in the feature table with their source databases:
Em., EMBL; Sw. SWISSPROT; Tr., TrEMBL; Wp., WORMPEP; Information on the WORMPEP database can be found at
http://www.sanger.ac.uk/Projects/C_elegans/wormpep This sequence was generated from part of bacterial clone contigs of human chromosome 1, constructed by the Sanger Centre Chromosome 1 Mapping Group. Further information can be found at
http://www.sanger.ac.uk/HGP/Chrl
RP11-142B3 is from the library RPCI-11.1 constructed by the group of Pieter de Jong. For further details see
http://www.chori.org/bacpac/home.htm
VECTOR: pBACe3.6
----- Genome Center
Center: Wellcome Trust Sanger Institute
Center code: SC
Web site: http://www.sanger.ac.uk
Contact: vegas@sanger.ac.uk

This sequence was finished as follows unless otherwise noted: all regions were either double-stranded or sequenced with an alternate chemistry or covered by high quality data (i.e., phred quality >= 30); an attempt was made to resolve all sequencing problems, such as compressions and repeats; all regions were covered by at least one subclone; and the assembly was confirmed by restriction digest, except on the rare occasion of the clone being a YAC.

FEATURES
source Location/Qualifiers
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/organism="Homo sapiens"

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/db_xref="taxon:9606"
/chromosome="1"
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/clone_lib="RPC1-11.1"
2000
/misc_feature
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24025..24029
/note="Sequence from uni-directional dGTP big dye
terminator reads only."
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AL035414.30:130672..130805,
complement(AL034351.1:124160..124227),
complement(AL034351.1:99498..99611),
complement(AL034351.1:86417..86611),
complement(AL034351.1:82400..82615),
complement(AL034351.1:68754..68925),
complement(AL034351.1:22424..22574),28075..28110,
102820..103021,AL691441.8:22351..22495,
complement(AC096636.1:134632..136640))
/gene="HHAT"
/locus_tag="RP11-7512.2-001"
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complement(AL034351.1:22424..22574),28075..28110,
102820..103021,AL691441.8:22351..22495,
complement(AC096636.1:134632..136640))
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complement(AL034351.1:124160..124227),
complement(AL034351.1:99498..99611),
complement(AL034351.1:86417..86611),
complement(AL034351.1:82400..82615),
complement(AL034351.1:68754..68925),
complement(AL034351.1:22424..22574),28075..28110,
102820..103021,AL691441.8:22351..22495,
complement(AC096636.1:134632..136640))
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102820..103021,AL691441.8:22351..22495,
complement(AC096636.1:134632..136640))
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/locus_tag="RP11-7512.2-001"
/product="hedgehog acyltransferase"
/note="match: CDNAs: Em:AK092186.1"
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AL035414.30:130672..130805,
complement(AL034351.1:124160..124227),
complement(AL034351.1:99498..99611),
complement(AL034351.1:86417..86611),
complement(AL034351.1:82400..82615),
complement(AL034351.1:68754..68925),
complement(AL034351.1:22424..22574),28075..28110,
102820..103021,AL691441.8:22351..22495,
complement(AC096636.1:134632..136640))
/gene="HHAT"
/translation="MLPFWELALYLASLGFHFYFYFYKYVKSREHEELDQSFLELT
DTLFGCLKDADTFMSFMWKGQWLVLLGLHMVVSQMATLLARKRPWILMLYGM
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KTENEYLLAQFTLVRCLYTTSFSLCHCQQLPAASTSYSPFPMLAYFYFVPLRHGP
ILSFSEPIKMQCQOQEHDSKASLCVLALGLGRLLCWWLAELMAHLMYHAIYSSIPL
LSTVSCWTLGLALAQVLFYFYKYLVLFGVPALLMLDLGTLTPPALPRCVSTWTFSTGM
WRYFDVGLHNFILRYIYIPVGSQHGLLGLTFLSTAMTFAFVSYWHGGYDLWCWAAIN
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EVGKTYMNRIFTQGWPMWTVLSVGLFYCYSHVGIWAQTYATD"
51012
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/locus_tag="RP11-7512.2-001"
/note="Clone_left_end: RP11-287C10"
59931..60045
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(AL451104) and RP11-208F18 (AL391594). Assembly confirmed
by restriction digest."
85506..85557
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/note="Sequence from overlapping clones RP11-287C10
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by restriction digest."
116103
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ORIGIN
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Best Local Similarity 54.5%; Pred. No. 15;
Matches 73; Conservative 0; Mismatches 61; Indels 0; Gaps 0;

QY 19 CTCACCTCGCTCAGCTATATAGAGAGCCCTCAACCAATTGAAATGCCCTCAACAGACGCTCAA 78
|||||
Db 2893 CTCCTAGCTCAGATGATACATTAGTTTCAATCATCTGCTGCTTCTCTCGTGGGATTCCC 2952
|||||
QY 79 AAGCTACAGACTATTTATCATATTTCTGCTCATCTTAATATGCTCTTCTGCTGATCTGT 138
|||||
Db 2953 ATGCATCTGTATGTAATAAATATTTTCTCTGTTAATCTGCTTATGCAATTTGT 3012
|||||
QY 139 ATCATCTGCTGATGCT 152
|||||
Db 3013 AGACCAAGATCCT 3026
|||||

RESULT 49
AC158428 136485 bp DNA linear HTG 13-JUL-2005
LOCUS Ornithorhynchus anatinus clone OA_Bb-338A1, WORKING DRAFT SEQUENCE,
DEFINITION 7 ordered pieces.
AC158428
AC158428.2 GI:70778563
VERSION HTG: HTGS_PHASE2: HTGS DRAFT.
KEYWORDS Ornithorhynchus anatinus (platypus)
SOURCE Ornithorhynchus anatinus
ORGANISM Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Monotremata; Ornithorhynchidae; Ornithorhynchus.
1 (bases 1 to 136485)
REFERENCE
AUTHORS Antonellis,A., Ayele,K., Baas,D., Benjamin,B., Bera,J.,
Blakesley,R.W., Bouffard,G.G., Brinkley,C., Brooks,S., Chu,G.,
Coleman,H., Engle,J., Fuxsenko,T., Gestole,M., Greene,A., Guan,X.,
Gupta,J., Haghighi,P., Han,J., Hansen,N., Ho,S.-L., Hu,P.,
Hunter,G., Hurlb,B., Idol,J.R., Kwong,P., Laric,P., Larson,S.,
Lee-Lin,S.-O., Legaspi,R., Madden,M., Maduro,Q.I., Maduro,V.B.,
Margulies,E.H., Masello,C., Maskeri,B., McDowell,J., Mojidi,H.A.,
Mullikin,J.C., Oestreicher,J.S., Park,M., Portnoy,M.E., Prasad,A.,
Puri,O., Reddx-Dugue,N., Sante,A., Schandler,K., Schueler,M.G.,
Sison,C., Stantropop,S., Stephen,E., Taye,A., Thomas,J.W.,
Thomas,P.J., Teipouri,V., Ung,L., Vogt,J.L., Wetherby,K.D.,
Withers,T.R., Young,A. and Green,E.D.
NISC Comparative Sequencing Initiative
Unpublished
2 (bases 1 to 136485)
Green,E.D.
Direct Submission
Submitted (16-MAR-2005) NIH Intramural Sequencing Center, 5625
Fishers Lane, Rockville, MD 20852, USA
3 (bases 1 to 136485)
Green,E.D.
Direct Submission
Submitted (13-JUL-2005) NIH Intramural Sequencing Center, 5625
Fishers Lane, Rockville, MD 20852, USA
On Jul 13, 2005 this sequence version replaced gi:61326072.

----- Genome Center
Center: NIH Intramural Sequencing Center
Center code: NISC
Web site: <http://www.nisc.nih.gov>
Contact: nisc.zoo@nhgri.nih.gov
----- Project Information
Center project name: jbm
Center clone name: 338A01

The sequence data in this record represents an 'enhanced'
version of a Phase 2 submission. Specifically, the indicated
order and orientation of each sequence contig has been
established using one or more of the following: read-pair
data from individual subclones, overlaps with neighboring
clones, alignment with available reference sequence (e.g.,
human), and/or confirmation by PCR testing. In addition,
the sequence assembly is generally based on at least 8X average
coverage in Q20 bases and has been reviewed to rule out

gross misassemblies, the low-quality ends of sequence
contigs have been trimmed away, and each base is associated
with a Phrap-derived quality score.
----- Summary Statistics -----
Sequencing vector: plasmid; n/a; 100% of reads
Chemistry: Dye-terminator Big Dye; version 0.990319
Assembly program: Phrap; version 0.990319
Consensus quality: 134683 bases at least Q40
Consensus quality: 135292 bases at least Q30
Consensus quality: 135669 bases at least Q20
Insert size: 139000; agarose-fp
Insert size: 135885; sum-of-contigs
Quality coverage: 9.53x in Q20 bases; agarose-fp
Quality coverage: 9.75x in Q20 bases; sum-of-contigs

* NOTE: This is a 'working draft' sequence. It currently
* consists of 7 contigs. Gaps between the contigs
* are represented as runs of N. The order of the pieces
* is believed to be correct as given, however the sizes
* of the gaps between them are based on estimates that have
* provided by the submitter.
* This sequence will be replaced
* by the finished sequence as soon as it is available and
* the accession number will be preserved.
* 1 13130: contig of 13130 bp in length
* 13131 13230: gap of unknown length
* 13231 25045: contig of 11815 bp in length
* 25046 25145: gap of unknown length
* 25146 64059: contig of 38914 bp in length
* 64060 64159: gap of unknown length
* 64160 70711: contig of 6552 bp in length
* 70712 70811: gap of unknown length
* 70812 76877: contig of 6066 bp in length
* 76878 108954: contig of 31977 bp in length
* 108955 109054: gap of unknown length
* 109055 136485: contig of 27431 bp in length.
Location/Qualifiers
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/mol_type="genomic DNA"
/db_xref="taxon:9258"
/clone="OA_Bb-338A1"
/clone_lib="OA_Bb"
1. .13130
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vector_side:left"
13131..13230
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13231..25045
/note="assembly_fragment"
25046..25145
/estimated_length=unknown
25146..64059
/note="assembly_fragment"
47918..136485
/note="clone overlaps with GenBank Accession Number
AC158266 clone OA_BB-408G4 (center project name jbl) "
64060..64159
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70812..76877
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76878..76977
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76978..108954
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108955..109054
/estimated_length=unknown
gap

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misc_feature      73879..74074
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misc_feature      74098
                    /note="Tandem repeat. Forced join. Gap size estimated to
                    be approximately 50bp by restriction digest data."
misc_feature      94364
                    /note="Clone_left_end: RP11-51P14"
misc_feature      141913
                    /note="Clone_right_end: RP11-520P22"

ORIGIN
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Best Local Similarity 53.2%; Pred. No. 27;
Matches 75; Conservative 0; Mismatches 66; Indels 0; Gaps 0;

QY      4      GAGAAAGTCCATACCTCACTCGCTCAGCTATATAGAGAGGCTCAACCAATTGAATGCCT 63
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Db      74705  GGGAACTCCAAAGCTGTACTCTACTCTGCATGTTGTGTTTACTCATTTGTCAGCTC 74646

QY      64      CAACAAGCACGTCAAAAGCTACAGAATCTATTATCAATTTCTGCTCATCTTAATATGT 123
          |||||
Db      74645  CCACATGTGAGTAAAGACATACAGTTTGTGACTCTCTGTTTCTGAGTCATTTCACTAAGG 74586

QY      124     CTCCTTGCTGATCTGTATCATC 144
          |||||
Db      74585  ATAATGGCCTCCAGTTTCACC 74565

Search completed: December 8, 2005, 01:11:23
Job time : 2067 secs

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Search completed: December 8, 2005, 01:11:23
Job time : 2067 secs

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ORIGIN
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Best Local Similarity 61.1%; Pred. No. 21;
Matches 58; Conservative 0; Mismatches 37; Indels 0; Gaps 0;
Qy 61 CCTCAACAGCAGCTCAAAAGTCACAGATCTATTATCAATTTCTCTCATCTTAATA 120
Db 9023 CCCCAAAACAAAGTTACTGCTGCAATTAATATTTTGGAGTTCTGCCCTTGCTTAATA 9082
Qy 121 TGTCTCTTGGTATCTGTATCATCGTGATGCTCT 155
Db 9083 TTTTCTCTGCTTGTTCATTATCAATCGATGCATAT 9117

RESULT 50
AL512452/c
LOCUS
DEFINITION
Human DNA sequence from clone Rpl11-520F22 on chromosome 13,
complete sequence.
ACCESSION
AL512452
VERSION
AL512452.7 GI:14252360
KEYWORDS
HTG.
SOURCE
Homo sapiens (human)
ORGANISM
Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Homnidae; Homo.
REFERENCE
1 (bases 1 to 141913)
AUTHORS
Tracev.A

```

REFERENCE
Hominidae; Homo.
1 (bases 1 to 141913)
TRACEV, A.
AUTHORS

TITLE	COMMENT
Direct Submission	
Submitted (13-MAY-2005)	Wellcome Trust Sanger Institute, Hinxton, Cambridgeshire, CB10 1SA, UK. E-mail enquiries: vega@sanger.ac.uk
Clone requests:	clonerequest@sanger.ac.uk
On May 30, 2001	this sequence version replaced gi:13398925.
The following abbreviations	are used to associate primary accession numbers given in the feature table with their source databases:
Em:, EMBL; Sw:, SWISSPROT; Tr:, TREMBL; Wp:, WORMPEP; Information	on the WORMPEP database can be found at
http://www.sanger.ac.uk/projects/C.elegans/wormpep	This sequence was generated from part of bacterial clone configs of human chromosome 13, constructed by the Sanger Centre Chromosome 13 Mapping Group. Further information can be found at
http://www.sanger.ac.uk/HGP/Chr13	
RP11-520F22	is from the library RP11-11.2 constructed by the group of Pieter de Jong. For further details see
http://www.chori.org/bacpac/home.htm	
VECTOR: pBAC3.6	
-----	Genome Center
Center: Wellcome Trust Sanger Institute	
Center code: SC	
Web site: http://www.sanger.ac.uk	
Contact: vega@sanger.ac.uk	

```

-----
This sequence was finished as follows unless otherwise noted: all
regions were either double-stranded or sequenced with an alternate
chemistry or covered by high quality data (i.e., phred quality >=
30); an attempt was made to resolve all sequencing problems, such
as compressions and repeats; all regions were covered by at least
one subclone; and the assembly was confirmed by restriction digest,
except on the rare occasion of the clone being a YAC.

Location/Qualifiers
1. 141913
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   /mol_type="genomic DNA"
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   /clone="RP11-520P22"
   /clone_lib="RPC1-11.2"

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GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: December 7, 2005, 20:37:40 ; Search time 479 Seconds

(without alignments)

2212.288 Million cell updates/sec

Title: US-10-691-412-1

Perfect score: 159

Sequence: 1 atggagaaagccaataacct.....tcacgtgatgcttctctga 159

Scoring table: IDENTITY NUC

Gapop 10.0 , Gapext 1.0

Searched: 4996997 seqs, 3332346308 residues

Total number of hits satisfying chosen parameters: 9993994

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 100 summaries

Database : N Geneseq_21.*

- 1: Geneseqn1980s.*
- 2: Geneseqn1990s.*
- 3: Geneseqn2000s.*
- 4: Geneseqn2001as.*
- 5: Geneseqn2001bs.*
- 6: Geneseqn2002as.*
- 7: Geneseqn2002bs.*
- 8: Geneseqn2003as.*
- 9: Geneseqn2003bs.*
- 10: Geneseqn2003cs.*
- 11: Geneseqn2003ds.*
- 12: Geneseqn2004as.*
- 13: Geneseqn2004bs.*
- 14: Geneseqn2005s.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	159	100.0	159	13	ADR97285 Human pho
2	159	100.0	480	3	AAC06724 Human sec
3	159	100.0	525	9	ACH16833 Human adu
4	159	100.0	1635	6	ABL61825 Colon ade
5	159	100.0	1635	12	ADN04087 Antipsori
6	159	100.0	1712	12	ADP21384 Gene PLN
7	159	100.0	1712	14	AEA81478 Human Pho
8	158	99.4	380	9	ACH16738 Human adu
9	158	99.4	418	9	ACH18023 Human adu
10	157.4	99.0	394	9	ACH17005 Human adu
11	147.8	93.0	487	9	ACH18165 Human adu
12	147.8	93.0	492	9	ACH30165 Human tes
13	144.6	90.9	407	9	ACH16630 Human adu
14	143	89.9	159	3	AAC64967 Pig phosph
15	127.6	80.3	306	6	ABN22344 Human ORF
16	123.8	77.9	701	10	ABE53082 Primary r
17	83	52.2	312	3	AAZ50498 KDEL rece
18	46	28.9	108	13	ADS18082 Human/mou
19	46	28.9	108	13	ADS18083 Human/mou

C	20	46	28.9	135	13	ADS18085	Adsl8085 Mouse AIP
C	21	46	28.9	135	13	ADS18084	Adsl8084 Mouse AIP
C	22	34.8	21.9	101169	12	ADQ97584	Adq97584 Mouse can
C	23	34.6	21.8	2043	2	AAX59526	Aax59526 DNA encod
C	24	34.6	21.8	2071	2	AAV46494	Aav46494 Interleuk
C	25	33.4	21.0	37973	6	ABL34196	Ab134196 Human imm
C	26	33.2	20.9	80268	13	ABD32951	Abd32951 Mouse can
C	27	32.6	20.5	170279	13	ABD32686	Abd32686 Mouse can
C	28	32.2	20.3	3713	2	AAQ64111	Aaq64111 cryET4 ge
C	29	32.2	20.3	3713	2	AAT95050	Aat95050 DNA encod
C	30	32.2	20.3	3713	2	AAT68435	Aat68435 CryET4 ge
C	31	32.2	20.3	3713	2	AAV83926	Aav83926 DNA encod
C	32	32.2	20.3	3713	2	AAZ09159	Aaz09159 B. thurin
C	33	32.2	20.3	127432	12	AD043653	Ado43653 Nucleotid
C	34	32	20.1	1590	12	ADN73394	Adn73394 Thale cre
C	35	31.8	20.0	1421	2	AAV74594	Aav74594 Staphyloc
C	36	31.8	20.0	6025	14	ADM94142	Adm94142 Staphyloc
C	37	31.4	19.7	873	5	AAS69551	Aas69551 DNA encod
C	38	31.4	19.7	873	5	AAS69244	Aas69244 DNA encod
C	39	31.4	19.7	873	5	AAS75469	Aas75469 DNA encod
C	40	31.4	19.7	2000	11	ACL38668	ACL38668 Rice stre
C	41	31.4	19.7	3505	4	ABL19916	Ab119916 Drosophil
C	42	31.4	19.7	5875	6	ABL32288	Ab132288 Human imm
C	43	31.2	19.6	84073	11	ACN44322	Acn44322 Human gen
C	44	31	19.5	1269	13	ADR60694	Adr60694 Cotton CD
C	45	31	19.5	6182	6	ABL34015	Ab134015 Human imm
C	46	31	19.5	271990	10	ADD25213	Add25213 Fertility
C	47	31	19.5	271990	12	ADM61228	Adm61228 Radish nu
C	48	30.8	19.4	437	13	ADR61212	Adr61212 Cotton CD
C	49	30.8	19.4	2090	2	AAQ62612	Aaq62612 Human mdr
C	50	30.8	19.4	3060	14	ADY95063	Ady95063 Multi-dru
C	51	30.8	19.4	3060	14	ADZ26757	Adz26757 Graft ver
C	52	30.8	19.4	8573	6	ABS98184	Abs98184 Human mul
C	53	30.8	19.4	10200	6	AAD41243	Aad41243 Human MDR
C	54	30.8	19.4	177380	8	ACF62751	Acf62751 Cancer ba
C	55	30.8	19.4	177380	8	ADB20870	Adb20870 MRP1 base
C	56	30.8	19.4	177380	10	ADB87959	Adb87959 Human UGT
C	57	30.8	19.4	177380	10	ADB96942	Adb96942 Human MDR
C	58	30.8	19.4	177380	10	ADB92133	Adb92133 Human MDR
C	59	30.6	19.2	349	8	ABX36263	Abx36263 Bovine ES
C	60	30.6	19.2	496	9	ACH37982	Ach37982 Human end
C	61	30.6	19.2	551	6	ABL83073	Ab183073 Human ova
C	62	30.6	19.2	930	4	AAS30994	Aas30994 Human dia
C	63	30.6	19.2	1132	4	AAS34823	Aas34823 cDNA enco
C	64	30.6	19.2	1132	10	ADC45981	Adc45981 Human neo
C	65	30.6	19.2	1434	4	AAI59427	Aai59427 Human pol
C	66	30.6	19.2	1592	4	AAH14974	Aah14974 Human CDN
C	67	30.6	19.2	1973	5	ADL61951	Adl61951 Human ova
C	68	30.6	19.2	2571	4	AAI61213	Aai61213 Human pol
C	69	30.6	19.2	2615	5	AAD02597	Aad02597 Human Ele
C	70	30.6	19.2	2617	13	ADR66787	Adr66787 Human pro
C	71	30.6	19.2	2617	13	ADR65884	Adr65884 Human pro
C	72	30.6	19.2	89873	13	ABD32846	Abd32846 Mouse can
C	73	30.6	19.2	95109	6	ABQ99654	Abq99654 Human mem
C	74	30.4	19.1	371	4	AAH29590	Aah29590 Drosophil
C	75	30.4	19.1	1209	10	ADF73039	Adf73039 NYD-Sp17
C	76	30.2	19.0	277	6	ABL72882	Ab172882 Corn tass
C	77	30.2	19.0	612	5	ABV06511	Abv06511 Human pro
C	78	30.2	19.0	18678	4	AAK91271	Aak91271 Human dig
C	79	30.2	19.0	18678	4	AAS32889	Aas32889 Human gen
C	80	30.2	19.0	25002	6	ABQ74278	Abq74278 C. elegan
C	81	30.2	19.0	25002	12	AD127983	Ad127983 Nematode
C	82	30.2	19.0	34203	11	ACN45106	Acn45106 Human gen
C	83	30.2	19.0	110000	10	ACF42745_2	Continuation (3 of
C	84	30.2	19.0	110000	13	ABD32966_04	Continuation (5 of
C	85	30.2	19.0	110000	13	ABD32966_05	Continuation (6 of
C	86	30.2	19.0	198073	11	ACN44302	Acn44302 Human gen
C	87	30	18.9	475	3	AAA43951	Aaa43951 Human sec
C	88	30	18.9	859	2	ACF62810	Adf62810 A. gossyp
C	89	30	18.9	2986	8	ACF62810	Adf62810 Colon can
C	90	30	18.9	3486	8	ABZ10140	Abz10140 Haematopo
C	91	30	18.9	3486	10	ABE54238	Adbe54238 Pretrate
C	92	30	18.9	3486	10	ADE84176	Ad84176 Human lym

c 93 30 18.9 3486 13 ADS89540
94 30 18.9 142519 10 AAD54634 Human chr
95 30 18.9 243390 13 ABD33366
96 30 18.9 243934 14 ADZ13446 Human can
97 29.8 18.7 413 6 ABN76328 Human ORF
c 98 29.8 18.7 711 6 ABS76838 Frog embr
99 29.8 18.7 765 13 ADR99954 Immune Re
100 29.8 18.7 972 14 ADV42443 Human psy

ALIGNMENTS

RESULT 1
ADR97285
ID ADR97285 standard; DNA; 159 BP.
XX AC ADR97285;
XX AC ADR97285;
DT 16-DEC-2004 (first entry)
XX DE Human phospholamban polymorphism fragment DNA.
XX KW ds; human; phospholamban; polymorphism; cardiovascular disease.
XX OS Homo sapiens.
XX PN US2004191802-A1.
XX PD 30-SEP-2004.
XX PF 22-OCT-2003; 2003US-00691412.
XX PR 22-OCT-2002; 2002US-0420295P.
XX PA (KRAN/) KRANIAS E G.
XX PA (HAGH/) HAGHIGHI K.
XX PI Kranias EG, Haghighi K;
XX WPI; 2004-689841/67.
XX PT Phospholamban polymorphism assessment in individual, for determining risk
PT for developing cardiovascular disease, by comparing analysis of the
PT nucleotide fragment with a predetermined phospholamban nucleotide
PT fragment sequence.
XX PS Claim 15; SEQ ID NO 1; 15pp; English.
XX CC The invention relates to a method of phospholamban polymorphism
CC assessment in an individual which comprises comparing the analysis of the
CC nucleotide fragment with a predetermined phospholamban nucleotide
CC fragment sequence to determine whether the individual carries a
CC phospholamban polymorphism. The methods and phospholamban polymorphism
CC fragment are useful for determining if an individual is at risk for
CC developing a cardiovascular disease. The present sequence represents the
CC human phospholamban polymorphism fragment DNA.

XX SQ Sequence 159 BP; 48 A; 39 C; 24 G; 48 T; 0 U; 0 Other;

Query Match 100.0%; Score 159; DB 13; Length 159;
Best Local Similarity 100.0%; Pred. No. 9e-39;
Matches 159; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ATGGAGAAAGTCCAAATACCTCAGCTCGCTATAGAAGAGCCTCAACCAATTGAATG 60
DB 1 ATGGAGAAAGTCCAAATACCTCAGCTCGCTATAGAAGAGCCTCAACCAATTGAATG 60
QY 61 CCTCAACAGCACGTCAAAAGCTACAGAACTATTATCAATTTCTGCTCATCTTAATA 120
DB 61 CCTCAACAGCACGTCAAAAGCTACAGAACTATTATCAATTTCTGCTCATCTTAATA 120

QY 121 TGTCTCTTGTGATCTGTATCATCGTGATGCTTCTCTGA 159

DB 121 TGTCTCTTGTGATCTGTATCATCGTGATGCTTCTCTGA 159
RESULT 2
AAC06724
ID AAC06724 standard; cDNA; 480 BP.
XX AC AAC06724;
XX DT 06-OCT-2000 (first entry)
XX DE Human secreted protein 5' EST, SEQ ID NO: 10799.
XX KW Human; 5' EST; expressed sequence tag; secreted protein; cDNA isolation;
XX KW gene therapy; chromosome mapping; ss.
XX OS Homo sapiens.
XX PN EP1033401-A2.
XX PD 06-SEP-2000.
XX PF 21-FEB-2000; 2000EP-00200610.
XX PR 26-FEB-1999; 99US-0122487P.
XX PA (GEST) GENSET.
XX PI Dumas Milne Edwards J, Duclert A, Giordano J;
XX WPI; 2000-500381/45.
XX PT New nucleic acid that is a 5' expressed sequence tag (5' EST) for
PT obtaining cDNAs and genomic DNAs that correspond to 5'ESTs and for
PT diagnostic, forensic, gene therapy and chromosome mapping procedures.
XX PS Claim 1; SEQ ID NO 10799; 71pp + Sequence Listing; English.
XX CC The present sequence is one of a large number of 5' ESTs derived from
CC mRNAs encoding secreted proteins. No ORF has yet been conclusively
CC identified within the present sequence. The 5' ESTs were prepared from
CC total human RNAs or polyA+ RNAs derived from 30 different tissues. EST
CC sequences usually correspond mainly to the 3' untranslated region (UTR)
CC of the mRNA because they are often obtained from oligo-dT primed cDNA
CC libraries. Such ESTs are not well suited for isolating cDNA sequences
CC derived from the 5' ends of mRNAs and even in those cases where longer
CC cDNA sequences have been obtained, the full 5' UTR is rarely included. 5'
CC ESTs are derived from mRNAs with intact 5' ends and can therefore be used
CC to obtain full length cDNAs and genomic DNAs. 5' ESTs are also used in
CC diagnostic, forensic, gene therapy and chromosome mapping procedures.
CC They are used to obtain upstream regulatory sequences and to design
CC expression and secretion vectors
XX SQ Sequence 480 BP; 149 A; 120 C; 76 G; 135 T; 0 U; 0 Other;
Query Match 100.0%; Score 159; DB 3; Length 480;
Best Local Similarity 100.0%; Pred. No. 1.3e-38;
Matches 159; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ATGGAGAAAGTCCAAATACCTCAGCTCGCTATAGAAGAGCCTCAACCAATTGAATG 60
DB 196 ATGGAGAAAGTCCAAATACCTCAGCTCGCTATAGAAGAGCCTCAACCAATTGAATG 255
QY 61 CCTCAACAGCACGTCAAAAGCTACAGAACTATTATCAATTTCTGCTCATCTTAATA 120
DB 256 CCTCAACAGCACGTCAAAAGCTACAGAACTATTATCAATTTCTGCTCATCTTAATA 315
QY 121 TGTCTCTTGTGATCTGTATCATCGTGATGCTTCTCTGA 159
DB 316 TGTCTCTTGTGATCTGTATCATCGTGATGCTTCTCTGA 354

RESULT 3
ACH16833
ID ACH16833 standard; cDNA; 525 BP.
XX
XX ACH16833;
XX
XX 13-OCT-2003 (first entry)
XX
XX Human adult heart cDNA #1147.
XX
XX Human; ss; sequencing by hybridisation; SBH; expressed sequence tag; EST;
XX genome mapping; biodiversity; genetic disorder.
XX
XX Homo sapiens.
XX
XX US2003073623-A1.
XX
XX 17-APR-2003.
XX
XX 30-JUL-2001; 2001US-00918995.
XX
XX 30-JUL-2001; 2001US-00918995.
XX
XX (DRMA/) DRMANAC R T.
XX (LABA/) LABAT I.
XX (STAC/) STACHE-CRAIN B.
XX (DICK/) DICKSON M C.
XX (JONE/) JONES L W.
XX
XX Drmanac RT, Labat I, Stache-Crain B, Dickson MC, Jones LW;
XX WPI; 2003-615964/58.
XX
XX New polynucleotide sequences obtained from various cDNA libraries, useful
XX as hybridization probes, as oligomers for PCR, for chromosome and gene
XX mapping, in the recombinant production of protein, or in generating
XX antisense DNA or RNA.
XX
XX Claim 1; SEQ ID NO 4045; 44bp; English.
XX
XX The invention relates to an isolated polynucleotide comprising any one of
XX 38043 cDNA sequences, appearing as ACH12789-ACH50831, whose sequence was
XX determined by the technique of SBH (sequencing by hybridisation). Also
XX included is a purified polypeptide comprising a sequence corresponding to
XX a reading frame of the novel polynucleotide. The nucleic acid sequences
XX are useful in diagnostics as expressed sequence tags (EST) for
XX identifying expressed genes or for physical mapping of the human genome,
XX in forensics, in assessing biodiversity, or in identifying mutations
XX responsible for genetic disorders and other traits. The nucleotide
XX sequences are also useful as hybridisation probes, as oligomers for PCR,
XX for chromosome and gene mapping, in the recombinant production of
XX protein, or in generating antisense DNA or RNA. The purified polypeptide
XX is useful for generating antibodies specific for it. The present sequence
XX is one of the 38043 isolated cDNA/EST sequences. Note: The sequence data
XX for this patent did not form part of the printed specification, but was
XX obtained in electronic format directly from USPTO at
XX seqdata.uspto.gov/sequence.html?DocID=20030073623
XX
XX Sequence 525 BP; 150 A; 153 C; 80 G; 140 T; 0 U; 2 Other;
XX
XX Query Match 100.0%; Score 159; DB 9; Length 525;
XX Best Local Similarity 100.0%; Pred. No. 1.3e-38;
XX Matches 159; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
XX 1 ATGGAGAAAGTCAATCACTCGCTCAGCTATAAGAGAGCCCTCAACCAATTGAATG 60
XX
XX 310 ATGGAGAAAGTCAATCACTCGCTCAGCTATAAGAGAGCCCTCAACCAATTGAATG 369
XX
XX 61 CCTCAACAGCAGCGTCAAGAGTACAGATCTATTATCAATTTCTGCTCATCTTAATA 120
XX
XX 370 CCTCAACAGCAGCGTCAAGAGTACAGATCTATTATCAATTTCTGCTCATCTTAATA 429
XX
XX 121 TGTCTCTTGCTGATCTGATCATCATGATGCTTCTCTGA 159

Db 430 TGTCTCTTGCTGATCTGATCATCATGATGCTTCTCTGA 468
RESULT 4
ABL61825
ID ABL61825 standard; DNA; 1635 BP.
XX
XX ABL61825;
XX
XX 15-MAY-2002 (first entry)
XX
XX Colon adenocarcinoma related gene sequence SEQ ID NO:162.
XX
XX Human; cancer; colon; breast; ovary; oesophagus; kidney; thyroid;
XX stomach; lung; prostate; pancreas; carcinoma; antitumour; cancerous;
XX KW cytostatic; Gene therapy; antineoplastic; Wilm's tumour; adenocarcinoma;
XX gene; ds.
XX
XX Homo sapiens.
XX
XX WO200194629-A2.
XX
XX 13-DEC-2001.
XX
XX 30-MAY-2001; 2001WO-US010838.
XX
XX 05-JUN-2000; 2000US-0209473P.
XX 05-JUN-2000; 2000US-0209531P.
XX 18-SEP-2000; 2000US-0233133P.
XX 18-SEP-2000; 2000US-0233617P.
XX 20-SEP-2000; 2000US-0234009P.
XX 20-SEP-2000; 2000US-0234034P.
XX 20-SEP-2000; 2000US-0234052P.
XX 22-SEP-2000; 2000US-0234509P.
XX 22-SEP-2000; 2000US-0234567P.
XX 25-SEP-2000; 2000US-0234923P.
XX 25-SEP-2000; 2000US-0234924P.
XX 25-SEP-2000; 2000US-0235077P.
XX 25-SEP-2000; 2000US-0235082P.
XX 25-SEP-2000; 2000US-0235134P.
XX 25-SEP-2000; 2000US-0235280P.
XX 26-SEP-2000; 2000US-0235637P.
XX 26-SEP-2000; 2000US-0235638P.
XX 27-SEP-2000; 2000US-0235711P.
XX 27-SEP-2000; 2000US-0235720P.
XX 27-SEP-2000; 2000US-0235840P.
XX 27-SEP-2000; 2000US-0235863P.
XX 28-SEP-2000; 2000US-0236028P.
XX 28-SEP-2000; 2000US-0236032P.
XX 28-SEP-2000; 2000US-0236033P.
XX 28-SEP-2000; 2000US-0236034P.
XX 28-SEP-2000; 2000US-0236109P.
XX 28-SEP-2000; 2000US-0236111P.
XX 29-SEP-2000; 2000US-0236842P.
XX 29-SEP-2000; 2000US-0236891P.
XX 02-OCT-2000; 2000US-0237172P.
XX 02-OCT-2000; 2000US-0237173P.
XX 02-OCT-2000; 2000US-0237278P.
XX 02-OCT-2000; 2000US-0237294P.
XX 02-OCT-2000; 2000US-0237295P.
XX 02-OCT-2000; 2000US-0237316P.
XX 03-OCT-2000; 2000US-0237425P.
XX 03-OCT-2000; 2000US-0237598P.
XX 03-OCT-2000; 2000US-0237604P.
XX 03-OCT-2000; 2000US-0237606P.
XX 03-OCT-2000; 2000US-0237608P.
XX 01-NOV-2000; 2000US-0244867P.
XX 01-NOV-2000; 2000US-0245084P.
XX
XX (AVAL-) AVALON PHARM.
XX
XX Young PE, Augustus M, Carter KC, Ebner R, Endress G, Horrigan S;
PI

PI Soppet DR, Weaver Z;
 XX WPI; 2002-188264/24.
 XX Screening for anti-neoplastic agent involves exposing cells to a chemical
 PT agent to be tested for anti-neoplastic activity, and determining a change
 PT in expression of a gene of a signature gene set.
 XX
 XX Claim 1; SEQ ID NO 162; 44pp; English.
 XX
 XX The present invention describes a method (M1) for screening for an anti-
 CC neoplastic agent. The method involves exposing cells to a chemical agent
 CC to be tested for anti-neoplastic activity, determining a change in
 CC expression of at least one gene (I) of a signature gene set, where (I)
 CC comprises a sequence (S) selected from 8447 sequences (given in AB61664
 CC to ABL70110), or is at least 95% identical to (S), where a change in
 CC expression is indicative of anti-neoplastic activity. (I) has cytostatic
 CC activity and can be used in gene therapy. M1 can be used for screening an
 CC anti-neoplastic agent, and can be used for producing a product which is
 CC the data collected with respect to the anti-neoplastic agent as a result
 CC of M1, and the data is sufficient to convey the chemical structure and/or
 CC properties of the agent. M1 can be used in the treatment of cancer such
 CC as colon, breast, stomach, lung, thyroid, oesophageal, ovarian, kidney,
 CC prostate or pancreatic cancer, adenocarcinoma, carcinoma, clear cell
 CC cancer, infiltrating ductal cancer, infiltrating lobular cancer, squamous
 CC cell carcinoma, neuroendocrine carcinoma, papillary carcinoma and Wilms's
 CC tumour
 XX
 XX Sequence 1635 BP; 567 A; 309 C; 231 G; 528 T; 0 U; 0 Other;
 Query Match 100.0%; Score 159; DB 6; Length 1635;
 Best Local Similarity 100.0%; Pred. No. 1.8e-38;
 Matches 159; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 ATGGAGAAAGTCCAAATACCTCACTCGCTCAGCTATAGAAGAGCGCTCAACCAATTGAAATG 60
 DB 182 ATGGAGAAAGTCCAAATACCTCACTCGCTCAGCTATAGAAGAGCGCTCAACCAATTGAAATG 241
 QY 61 CCTCAACAGCAGCGTCAAAAGCTACAGAAATCTATTTATCAATTTCTGCTCATCTTAATA 120
 DB 242 CCTCAACAGCAGCGTCAAAAGCTACAGAAATCTATTTATCAATTTCTGCTCATCTTAATA 301
 QY 121 TGTCTCTTGTGATCTGTATCATCGTGATCGTCTCTCTGA 159
 DB 302 TGTCTCTTGTGATCTGTATCATCGTGATCGTCTCTCTGA 340
 RESULT 5
 ADN04087
 ID ADN04087 standard; cDNA; 1635 BP.
 XX
 XX ADN04087;
 XX
 XX 01-JUL-2004 (first entry)
 XX
 XX Antipsoriatic cDNA sequence #243.
 XX
 XX ds; gene; antipsoriatic; gene therapy; psoriasis; diagnosis.
 XX
 XX Homo sapiens.
 XX
 XX WO2004028479-A2.
 XX
 XX 08-APR-2004.
 XX
 XX 25-SEP-2003; 2003WO-US030907.
 XX
 XX 25-SEP-2002; 2002US-0414006P.
 XX
 XX (GETH) GENENTECH INC.
 XX
 XX Bodary S, Clark H, Jackman J, Schoenfeld J, Williams PM, Wood WI;
 PI Wu TD;

XX WPI; 2004-305105/28.
 DR P-PSDB; ADN04088.
 XX
 XX New PRO nucleic acid or polypeptide, useful for preparing a
 PT pharmaceutical composition for diagnosing or treating psoriasis in a
 PT mammal.
 XX
 XX Claim 1; SEQ ID NO 481; 3069pp; English.
 XX
 XX The invention relates to novel polynucleotide and polypeptides for
 CC treating psoriasis or a sequence having at least 80% identity to the
 CC above sequences. The nucleic acid is useful for preparing a composition
 CC for diagnosing or treating psoriasis in a mammal. This sequence
 CC corresponds to one of the polynucleotides of the invention.
 XX
 XX Sequence 1635 BP; 567 A; 309 C; 231 G; 528 T; 0 U; 0 Other;
 Query Match 100.0%; Score 159; DB 12; Length 1635;
 Best Local Similarity 100.0%; Pred. No. 1.8e-38;
 Matches 159; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 ATGGAGAAAGTCCAAATACCTCACTCGCTCAGCTATAGAAGAGCGCTCAACCAATTGAAATG 60
 DB 182 ATGGAGAAAGTCCAAATACCTCACTCGCTCAGCTATAGAAGAGCGCTCAACCAATTGAAATG 241
 QY 61 CCTCAACAGCAGCGTCAAAAGCTACAGAAATCTATTTATCAATTTCTGCTCATCTTAATA 120
 DB 242 CCTCAACAGCAGCGTCAAAAGCTACAGAAATCTATTTATCAATTTCTGCTCATCTTAATA 301
 QY 121 TGTCTCTTGTGATCTGTATCATCGTGATCGTCTCTCTGA 159
 DB 302 TGTCTCTTGTGATCTGTATCATCGTGATCGTCTCTCTGA 340
 RESULT 6
 ADP21384
 ID ADP21384 standard; DNA; 1712 BP.
 XX
 XX ADP21384;
 XX
 XX 09-SEP-2004 (first entry)
 XX
 XX Gene PLN for screening for cardiac therapeutic preparation.
 DE
 XX ds; cardiant; gene therapy; cardiac therapeutic preparation;
 KW beta-adrenergic receptor antagonist; endothelial receptor antagonist;
 KW calcium channel antagonist; phosphodiesterase inhibitor;
 KW angiotensin converting enzyme inhibitor; heart failure.
 XX
 XX Homo sapiens.
 XX
 XX WO2004050894-A2.
 XX
 XX 17-JUN-2004.
 XX
 XX 26-NOV-2003; 2003WO-US037927.
 XX
 XX 27-NOV-2002; 2002US-0429379P.
 PR 31-DEC-2002; 2002US-0437051P.
 PR 31-DEC-2002; 2002US-0437102P.
 XX
 XX (ARTE-) ARTESIAN THERAPEUTICS INC.
 XX
 XX Bednarik DP;
 XX
 XX WPI; 2004-450738/42.
 XX
 XX Screening potential therapeutic compounds for cardiac therapeutic
 PT preparations, useful for treating heart failure in a subject, comprises
 PT contacting a sample of cell or tissue with a compound and detecting gene
 PT expression level.
 XX

PS Claim 10; SEQ ID NO 58; 152pp; English.
 XX
 CC The invention relates to a method of screening potential therapeutic
 CC compounds for cardiac therapeutic preparations by contacting a sample
 CC comprising a cell or tissue with a potential therapeutic compound and
 CC detecting a level of expression of a gene that codes for a product
 CC encoded by a nucleic acid selected from 98 sequences given in the
 CC specification and its conservative variants, comparing the level of the
 CC expression of the gene to the level of expression of the gene in the
 CC absence of the compound, and identifying a potential therapeutic compound
 CC for use as a cardiac therapeutic preparation if the potential therapeutic
 CC compound affects the level of expression of the gene. The pharmaceutical
 CC composition or active agents (i.e., beta-adrenergic receptor antagonist,
 CC endothelial receptor antagonist, calcium channel antagonist,
 CC phosphodiesterase inhibitor, or angiotensin converting enzyme inhibitor)
 CC is useful for treating heart failure in a subject. This sequence
 CC represents one of the genes whose expression may be altered by the
 CC compounds detected by the screen of the invention.
 XX
 SQ Sequence 1712 BP; 618 A; 313 C; 240 G; 541 T; 0 U; 0 Other;
 Query Match 100.0%; Score 159; DB 12; Length 1712;
 Best Local Similarity 100.0%; Pred. No. 1.9e-38;
 Matches 159; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ATGAGAGAAAGTCCAAATACCTCACTCGCTCAGCTATAAGAGAGCCTCAACCAATTGAAATG 60
 DB 182 ATGAGAGAAAGTCCAAATACCTCACTCGCTCAGCTATAAGAGAGCCTCAACCAATTGAAATG 241
 QY 61 CCTCAACAAGCAGCTCAAAAGCTACAGAACTATTATCAATTTCTGCTCATCTTAATA 120
 DB 242 CCTCAACAAGCAGCTCAAAAGCTACAGAACTATTATCAATTTCTGCTCATCTTAATA 301
 QY 121 TGTCTCTTGTGATCTGTATCATCGTATCGTCTCTCTGA 159
 DB 302 TGTCTCTTGTGATCTGTATCATCGTATCGTCTCTCTGA 340

RESULT 7
 AEA81478
 ID AEA81478 standard; cDNA; 1712 BP.
 AC AEA81478;
 XX
 DT 08-SEP-2005 (first entry)
 XX Human Phospholamban cDNA.
 DE
 XX Anorectic; obesity; cachexia; anabolic; genetic marker; skeletal muscle;
 KW ss; gene; drug screening.
 KW
 XX Homo sapiens.
 OS
 XX EP1548131-A2.
 PN
 XX 29-JUN-2005.
 PD
 XX 15-DEC-2004; 2004EP-00029642.
 PF
 XX 22-DEC-2003; 2003EP-00104899.
 PR
 XX (HOFF) HOFFMANN LA ROCHE & CO AG F.
 PA (OSTE/) OSTENSON C.
 PA
 XX Clerc RG, Duchateau-Nguyen G, Gardes C, Mizrahi J, Ostenson C;
 PI WPI; 2005-460899/47.
 DR P-PSDB; AEA81486.
 DR
 XX Screening compounds that reduce and/or prevent obesity, and/or treat
 PT cachexia, by contacting a cell expressing down-regulated or up-regulated
 PT genes in skeletal muscle in obesity.
 PT
 XX

PS Claim 2; SEQ ID NO 1; 239pp; English.
 XX
 CC The invention relates to screening for compounds that reduce and/or
 CC prevent obesity comprising contacting a cell expressing any of 6 down-
 CC regulated or 2 up-regulated genes in skeletal muscle in obesity, and
 CC measuring the expression of the gene, or a polypeptide encoded by the
 CC gene, where a compound which up-regulates or down-regulates gene
 CC expression is a compound which causes an increase of expression of the
 CC gene or of the polypeptide encoded by the gene. Also included are
 CC screening for compounds that bind to a polypeptide with any of AEA81486-
 CC AEA81493 and AEA81521-AEA81547 (comprising contacting a compound with the
 CC polypeptide, and determining the ability of the compound to bind the
 CC polypeptide), a kit for screening for compounds that reduce and/or
 CC prevent obesity (comprising a polypeptide selected from any of AEA81486-
 CC AEA81493 and AEA81521-AEA81547), a compound identified by the method
 CC cited above and a pharmaceutical formulation for the modulation of body
 CC weight (comprising a compound that modulates the activity of a
 CC polypeptide selected from AEA81486-AEA81493 and AEA81521-AEA81547, mixed
 CC with a pharmaceutical carrier). The genes or encoded polypeptides are
 CC useful as a target for screening of compounds that reduce and/or prevent
 CC obesity. The compound is useful in the preparation of a medicament for
 CC the treatment of obesity and/or cachexia. The present sequence is a cDNA
 CC from a human gene that is down regulated in skeletal muscle in obesity.
 XX
 SQ Sequence 1712 BP; 618 A; 313 C; 240 G; 541 T; 0 U; 0 Other;
 Query Match 100.0%; Score 159; DB 14; Length 1712;
 Best Local Similarity 100.0%; Pred. No. 1.9e-38;
 Matches 159; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ATGAGAGAAAGTCCAAATACCTCACTCGCTCAGCTATAAGAGAGCCTCAACCAATTGAAATG 60
 DB 182 ATGAGAGAAAGTCCAAATACCTCACTCGCTCAGCTATAAGAGAGCCTCAACCAATTGAAATG 241
 QY 61 CCTCAACAAGCAGCTCAAAAGCTACAGAACTATTATCAATTTCTGCTCATCTTAATA 120
 DB 242 CCTCAACAAGCAGCTCAAAAGCTACAGAACTATTATCAATTTCTGCTCATCTTAATA 301
 QY 121 TGTCTCTTGTGATCTGTATCATCGTATCGTCTCTCTGA 159
 DB 302 TGTCTCTTGTGATCTGTATCATCGTATCGTCTCTCTGA 340

RESULT 8
 ACH16738
 ID ACH16738 standard; cDNA; 380 BP.
 AC ACH16738;
 XX
 DT 13-OCT-2003 (first entry)
 XX Human adult heart cDNA #1052.
 DE
 XX Human; ss; sequencing by hybridisation; SBH; expressed sequence tag; EST;
 KW genome mapping; biodiversity; genetic disorder.
 KW
 XX Homo sapiens.
 OS
 XX US2003073623-A1.
 PN
 XX 17-APR-2003.
 PD
 XX 30-JUL-2001; 2001US-00918995.
 PF
 XX 30-JUL-2001; 2001US-00918995.
 PR
 XX (DRMA/) DRMANAC R T.
 PA (LABA/) LABAT I.
 PA (STAC/) STACHE-CRAIN B.
 PA (DICK/) DICKSON M C.
 PA (JONE/) JONES L W.
 XX
 PI Drmanac RT, Labat I, Stache-Crain B, Dickson MC, Jones LW;

(DICK//) DICKSON M C.
(JONE//) JONES L W.

Drmanac RT, Labat I, Stache-Crain B, Dickson MC, Jones LW;
WPI; 2003-615964/58.

New polynucleotide sequences obtained from various cDNA libraries, useful as hybridization probes, as oligomers for PCR, for chromosome and gene mapping, in the recombinant production of protein, or in generating antisense DNA or RNA.

Claim 1; SEQ ID NO 3950; 44pp; English.

The invention relates to an isolated polynucleotide comprising any one of 38043 cDNA sequences, appearing as ACH12789-ACH50831, whose sequence was determined by the technique of SBH (sequencing by hybridisation). Also included is a purified polypeptide comprising a sequence corresponding to a reading frame of the novel polynucleotide. The nucleic acid sequences are useful in diagnostics as expressed sequence tags (EST) for identifying expressed genes or for physical mapping of the human genome, in forensics, in assessing biodiversity, or in identifying mutations responsible for genetic disorders and other traits. The nucleotide sequences are also useful as hybridisation probes, as oligomers for PCR, for chromosome and gene mapping, in the recombinant production of protein, or in generating antisense DNA or RNA. The purified polypeptide is useful for generating antibodies specific for it. The present sequence is one of the 38043 isolated cDNA/EST sequences. Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from USPTO at seqdata.uspto.gov/sequence.html?DocID=20030073623

Sequence 380 BP; 110 A; 102 C; 54 G; 112 T; 0 U; 2 Other;
Query Match 99.4%; Score 158; DB 9; Length 380;
Best Local Similarity 99.4%; Pred. No. 2.4e-38;
Matches 158; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 ATGAGAAAGTCCAAATACCTCACTCGCTACGCTATAGAGAGCCTCAACCATTTGAATG 60
DB 182 ATGAGAAAGTCCAAATACCTCACTCGCTACGCTATAGAGAGCCTCAACCATTTGAATG 241

QY 61 CCTCAAGACGCTCAAAAGCTACAGAACTATTATCAATTTCTGTCTCATCTTAATA 120
DB 242 CCTCAAGACGCTCAAAAGCTACAGAACTATTATCAATTTCTGTCTCATCTTAATA 301

QY 121 TGTCTCTTGTGATCTGTATCATCTCGTATGCTTCTCTGA 159
DB 302 TGTCTCTTGTGATCTGTATCATCTCGTATGCTTCTCTGA 340

RESULT 9
ACH18023
ID ACH18023 standard; cDNA; 418 BP.
AC ACH18023;
XX
XX 13-OCT-2003 (first entry)
XX Human adult heart cDNA #2337.
XX
XX Human; ss; sequencing by hybridisation; SBH; expressed sequence tag; EST;
KW genome mapping; biodiversity; genetic disorder.
XX
XX Homo sapiens.
XX
XX US2003073623-A1.
XX
XX 17-APR-2003.
XX
XX 30-JUL-2001; 2001US-00918995.
XX
XX 30-JUL-2001; 2001US-00918995.
XX
XX (DRMA//) DRMANAC R T.
PA (LABA//) LABAT I.
PA (STAC//) STACHE-CRAIN B.

XX (DRMA/) DRMANAC R T.
PA (LABA/) LABAT I.
PA (STAC/) STACHE-CRAIN B.
PA (DICK/) DICKSON M C.
PA (JONE/) JONES L W.
XX
PI Drmanac RT, Labat I, Stache-Crain B, Dickson MC, Jones LW;
XX
XX WPI; 2003-615964/58.
XX
XX New polynucleotide sequences obtained from various cDNA libraries, useful
PT as hybridization probes, as oligomers for PCR, for chromosome and gene
PT mapping, in the recombinant production of protein, or in generating
PT antisense DNA or RNA.
XX
XX Claim 1; SEQ ID NO 4217; 44pp; English.
XX
XX The invention relates to an isolated polynucleotide comprising any one of
CC 38043 cDNA sequences, appearing as ACH12789-ACH50831, whose sequence was
CC determined by the technique of SBH (sequencing by hybridisation). Also
CC included is a purified polypeptide comprising a sequence corresponding to
CC a reading frame of the novel polynucleotide. The nucleic acid sequences
CC are useful in diagnostics as expressed sequence tags (EST) for
CC identifying expressed genes or for physical mapping of the human genome,
CC in forensics, in assessing biodiversity, or in identifying mutations
CC responsible for genetic disorders and other traits. The nucleotide
CC sequences are also useful as hybridisation probes, as oligomers for PCR,
CC for chromosome and gene mapping, in the recombinant production of
CC protein, or in generating antisense DNA or RNA. The purified polypeptide
CC is useful for generating antibodies specific for it. The present sequence
CC is one of the 38043 isolated cDNA/EST sequences. Note: The sequence data
CC for this patent did not form part of the printed specification, but was
CC obtained in electronic format directly from USPTO at
CC seqdata.uspto.gov/sequence.html?DocID=20030073623
XX
XX SQ Sequence 394 BP; 115 A; 107 C; 58 G; 113 T; 0 U; 1 Other;
XX
XX Query Match 99.0%; Score 157.4; DB 9; Length 394;
XX Best Local Similarity 99.4%; Pred. No. 3.7e-39;
XX Matches 158; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
XX
XX QY 1 ATGGAGAAAGTCCAATACCTCACTCGCTCAGCTATAGAGAGAGCTCAACCATTTGAAATG 60
XX Db 182 ATGGAGAAAGTCCAATACCTCACTCGCTCAGCTATAGAGAGAGCTCAACCATTTGAAATG 241
XX
XX QY 61 CCTCAACAGCAGCTCAAAAGCTACAGATCTATTATCAATTTCTGCTCATCTTAATA 120
XX Db 242 CCTCAACAGCAGCTCAAAAGCTACAGATCTATTATCAATTTCTGCTCATCTTAATA 301
XX
XX QY 121 TGTCTCTTCTGATCTGTATCATCGTGATGCTTCTCTGA 159
XX Db 302 TGTCTCTTCTGATCTGTATCATCGTGATGCTTCTCTGA 340
XX
XX RESULT 11
XX ACH18165
XX ID ACH18165 standard; cDNA; 487 BP.
XX
XX AC ACH18165;
XX
XX XX
XX DT 13-OCT-2003 (first entry)
XX
XX DE Human adult heart cDNA #2479.
XX
XX XX
XX KW Human; ss; sequencing by hybridisation; SBH; expressed sequence tag; EST;
XX genome mapping; biodiversity; genetic disorder.
XX
XX OS Homo sapiens.
XX
XX XX
XX FN US2003073623-A1.
XX
XX XX
XX PD 17-APR-2003.

XX 30-JUL-2001; 2001US-00918995.
XX
XX 30-JUL-2001; 2001US-00918995.
XX
XX (DRMA/) DRMANAC R T.
XX
XX (LABA/) LABAT I.
XX
XX (STAC/) STACHE-CRAIN B.
XX
XX (DICK/) DICKSON M C.
XX
XX (JONE/) JONES L W.
XX
XX
XX Drmanac RT, Labat I, Stache-Crain B, Dickson MC, Jones LW;
XX
XX WPI; 2003-615964/58.
XX
XX New polynucleotide sequences obtained from various cDNA libraries, useful
PT as hybridization probes, as oligomers for PCR, for chromosome and gene
PT mapping, in the recombinant production of protein, or in generating
PT antisense DNA or RNA.
XX
XX Claim 1; SEQ ID NO 5377; 44pp; English.
XX
XX The invention relates to an isolated polynucleotide comprising any one of
CC 38043 cDNA sequences, appearing as ACH12789-ACH50831, whose sequence was
CC determined by the technique of SBH (sequencing by hybridisation). Also
CC included is a purified polypeptide comprising a sequence corresponding to
CC a reading frame of the novel polynucleotide. The nucleic acid sequences
CC are useful in diagnostics as expressed sequence tags (EST) for
CC identifying expressed genes or for physical mapping of the human genome,
CC in forensics, in assessing biodiversity, or in identifying mutations
CC responsible for genetic disorders and other traits. The nucleotide
CC sequences are also useful as hybridisation probes, as oligomers for PCR,
CC for chromosome and gene mapping, in the recombinant production of
CC protein, or in generating antisense DNA or RNA. The purified polypeptide
CC is useful for generating antibodies specific for it. The present sequence
CC is one of the 38043 isolated cDNA/EST sequences. Note: The sequence data
CC for this patent did not form part of the printed specification, but was
CC obtained in electronic format directly from USPTO at
CC seqdata.uspto.gov/sequence.html?DocID=20030073623
XX
XX SQ Sequence 487 BP; 135 A; 140 C; 87 G; 122 T; 0 U; 3 Other;
XX
XX Query Match 93.0%; Score 147.8; DB 9; Length 487;
XX Best Local Similarity 95.6%; Pred. No. 3.4e-35;
XX Matches 152; Conservative 0; Mismatches 7; Indels 0; Gaps 0;
XX
XX QY 1 ATGGAGAAAGTCCAATACCTCACTCGCTCAGCTATAGAGAGAGCTCAACCATTTGAAATG 60
XX Db 252 ATGGAGAAAGTCCAATACCTCACTCGCTCAGCTATAGAGAGAGCTCAACCATTTGAAATG 311
XX
XX QY 61 CCTCAACAGCAGCTCAAAAGCTACAGATCTATTATCAATTTCTGCTCATCTTAATA 120
XX Db 312 CCTCAACAGCAGCTCAAAAGCTACAGATCTATTATCAATTTCTGCTCATCTTAATA 371
XX
XX QY 121 TGTCTCTTCTGATCTGTATCATCGTGATGCTTCTCTGA 159
XX Db 372 TGTCTCTTCTGATCTGTATCATCGTGATGCTTCTCTGA 410
XX
XX RESULT 12
XX ACH30165
XX ID ACH30165 standard; cDNA; 492 BP.
XX
XX AC ACH30165;
XX
XX XX
XX DT 13-OCT-2003 (first entry)
XX
XX DE Human testis cDNA #551.
XX
XX XX
XX KW Human; ss; sequencing by hybridisation; SBH; expressed sequence tag; EST;
XX genome mapping; biodiversity; genetic disorder.
XX
XX OS Homo sapiens.

Human, ss; sequencing by hybridisation; SBH; expressed sequence tag; EST; genome mapping; biodiversity; genetic disorder.

Homo sapiens.

US2003073623-A1.

17-APR-2003.

30-JUL-2001; 2001US-00918995.

30-JUL-2001; 2001US-00918995.

(DRMA/) DRMANAC R T.

(LABA/) LABAT I.

(STAC/) STACHE-CRAIN B.

(DICK/) DICKSON M C.

(JONE/) JONES L W.

Drmanac RT, Labat I, Stache-Crain B, Dickson MC, Jones LW;

WPI; 2003-615964/58.

New polynucleotide sequences obtained from various cDNA libraries, useful as hybridization probes, as oligomers for PCR, for chromosome and gene mapping, in the recombinant production of protein, or in generating antisense DNA or RNA.

Claim 1; SEQ ID NO 3842; 44pp; English.

The invention relates to an isolated polynucleotide comprising any one of 38043 cDNA sequences, appearing as ACH12789-ACH50831, whose sequence was determined by the technique of SBH (sequencing by hybridisation). Also included is a purified polypeptide comprising a sequence corresponding to a reading frame of the novel polynucleotide. The nucleic acid sequences are useful in diagnostics as expressed sequence tags (EST) for identifying expressed genes or for physical mapping of the human genome, in forensics, in assessing biodiversity, or in identifying mutations responsible for genetic disorders and other traits. The nucleotide sequences are also useful as hybridisation probes, as oligomers for PCR, for chromosome and gene mapping, in the recombinant production of protein, or in generating antibodies specific for it. The present sequence is one of the 38043 isolated cDNA/EST sequences. Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from USPTO at seqdata.uspto.gov/sequence.html?DocID=20030073623

Sequence 407 BP; 116 A; 102 C; 76 G; 113 T; 0 U; 0 Other;

Query Match 90.9%; Score 144.6; DB 9; Length 407;

Best Local Similarity 94.3%; Pred. No. 3.1e-34;

Matches 150; Conservative 0; Mismatches 9; Indels 0; Gaps 0;

Qy 1 ATGGAGAAAGTCCAAATACCTCAGCTATATAGAGAGCCTCAACCATTTGAATG 60

Db 182 ATGGAGAAAGTCCAAATACCTCAGCTATATAGAGAGCCTCAACCATTTGAATG 241

Qy 61 CCTCAACAAGCAGCTCAAAAGCTACAGAACTATTATCAATTTCTCTCATCTTAATA 120

Db 242 CCTCAGCAGCAGCCTCAAAAGCTACAGAACTATTATCAATTTCTCTCATCTTAATA 301

Qy 121 TGTCTCTTGTGATCTGTATCATCGTATGCTTCTCTGA 159

Db 302 TGTCTCTTGTGATCTGTATCATCGTATGCTTCTCTGA 340

RESULT 14

AAC64967

ID AAC64967 standard; cDNA; 159 BP.

XX AAC64967;

XX

XX

FN US2003073623-A1.

XX

PD 17-APR-2003.

XX

PF 30-JUL-2001; 2001US-00918995.

XX

PR 30-JUL-2001; 2001US-00918995.

XX

PA (DRMA/) DRMANAC R T.

PA (LABA/) LABAT I.

PA (STAC/) STACHE-CRAIN B.

PA (DICK/) DICKSON M C.

PA (JONE/) JONES L W.

XX

PI Drmanac RT, Labat I, Stache-Crain B, Dickson MC, Jones LW;

XX

DR WPI; 2003-615964/58.

XX

PT New polynucleotide sequences obtained from various cDNA libraries, useful as hybridization probes, as oligomers for PCR, for chromosome and gene mapping, in the recombinant production of protein, or in generating antisense DNA or RNA.

XX

PS Claim 1; SEQ ID NO 17377; 44pp; English.

XX

CC The invention relates to an isolated polynucleotide comprising any one of 38043 cDNA sequences, appearing as ACH12789-ACH50831, whose sequence was determined by the technique of SBH (sequencing by hybridisation). Also included is a purified polypeptide comprising a sequence corresponding to a reading frame of the novel polynucleotide. The nucleic acid sequences are useful in diagnostics as expressed sequence tags (EST) for identifying expressed genes or for physical mapping of the human genome, in forensics, in assessing biodiversity, or in identifying mutations responsible for genetic disorders and other traits. The nucleotide sequences are also useful as hybridisation probes, as oligomers for PCR, for chromosome and gene mapping, in the recombinant production of protein, or in generating antibodies specific for it. The present sequence is one of the 38043 isolated cDNA/EST sequences. Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from USPTO at seqdata.uspto.gov/sequence.html?DocID=20030073623

XX

SQ Sequence 492 BP; 141 A; 136 C; 88 G; 125 T; 0 U; 2 Other;

Query Match 93.0%; Score 147.8; DB 9; Length 492;

Best Local Similarity 95.6%; Pred. No. 3.4e-35;

Matches 152; Conservative 0; Mismatches 7; Indels 0; Gaps 0;

Qy 1 ATGGAGAAAGTCCAAATACCTCAGCTATATAGAGAGCCTCAACCATTTGAATG 60

Db 278 ATGGAGAAAGTCCAAATACCTCAGCTATATAGAGAGCCTCAACCATTTGAATG 337

Qy 61 CCTCAACAAGCAGCTCAAAAGCTACAGAACTATTATCAATTTCTCTCATCTTAATA 120

Db 338 CCTCAACAAGCAGCTCAAAAGCTACAGAACTATTATCAATTTCTCTCATCTTAATA 397

Qy 121 TGTCTCTTGTGATCTGTATCATCGTATGCTTCTCTGA 159

Db 398 TGTCTCTTGTGATCTGTATCATCGTATGCTTCTCTGA 436

RESULT 13

ACH16630

ID ACH16630 standard; cDNA; 407 BP.

XX ACH16630;

AC

XX 13-OCT-2003 (first entry)

DT

XX Human adult heart cDNA #944.

DE

XX

DT 09-FEB-2001 (first entry)
XX
DE Pig phospholamban cDNA.
XX
KW Pig: sarco/endoplasmic reticulum calcium ATPase; SERCA; signalling;
KW cardiac hypertrophy; heart failure; hypertension; Darter-White disease;
KW Brody's disease; diabetes; ss.
XX
OS Sus scrofa.
XX
PN GB2349217-A.
XX
PD 25-OCT-2000.
XX
PF 14-APR-2000; 2000GB-00009363.
XX
PR 15-APR-1999; 99GB-00008670.
XX
PR 15-APR-1999; 99US-0129596P.
XX
PR 01-JUN-1999; 99GB-00012736.
XX
XX (DEVG-) DEVGEN NV.
XX
PI Zwaal R, Groenen J, Bogaert T;
XX
XX WPI; 2000-658082/64.
XX
XX Identifying modulators of sarco/endoplasmic reticulum calcium ATPase,
XX useful potentially for treating disorders of calcium homeostasis, e.g.
XX cardiac hypertrophy.
XX
XX Disclosure; Fig 11; 108pp; English.
XX
XX The present invention is concerned with methods of using C. elegans to
XX identify compounds which are capable of up- and down-regulating the
XX activity of the sarco/endoplasmic reticulum calcium ATPase (SERCA). This
XX protein is involved in cell signalling, and elevated levels affect
XX cellular processes such as contraction, secretion and cell cycling. The
XX methods can be used to identify compounds for use in the treatment of
XX some muscle pathologies, cardiac hypertrophy, heart failure,
XX hypertension, diabetes, Darter-White disease and Brody's disease
XX
SQ Sequence 159 BP; 45 A; 41 C; 22 G; 51 T; 0 U; 0 Other;
Query Match 89.9%; Score 143; DB 3; Length 159;
Best Local Similarity 93.7%; Pred. No. 7.2e-34;
Matches 149; Conservative 0; Mismatches 10; Indels 0; Gaps 0;
QY 1 ATGGAGAAAGTCAATACCTCACTCGCTCAGTATGAAGAGCCCTCAACCAATTGAAATG 60
DB 1 ATGGATAAAGTCCAAATACCTCACTCGCTCTGCTATTAGAGAGCTTCAACCAATTGAAATG 60
QY 61 CCTCAACAAGCAGCTCAAAAGCTACAGNATCTATTATCAATTTCTGCTCATCTTAATA 120
DB 61 CCTCAACAAGCAGCTCAAAAGCTTCAAGAACCTTATTAATCAATTTCTGCTCATCTTAATA 120
QY 121 TGTCTCTTGTGATCTGTATCATCGTGTGATGCTTCTCTGA 159
DB 121 TGGCTCTTGTGATTTGATTCATCATCGTGTGATGCTTCTCTGA 159
RESULT 15
ABN22344
ID ABN22344 standard; cDNA; 306 BP.
XX
AC ABN22344;
XX
XX 24-JUN-2002 (first entry)
DT Human ORFX polynucleotide sequence SEQ ID NO:13165.
DE Human; open reading frame; ORFX; gene therapy; cancer; cirrhosis;
KW hyperproliferative disorder; psoriasis; benign tumour; haemorrhage;
KW degenerative disorder; osteoarthritis; neurodegenerative disorder;
KW

KW cardiovascular disease; diabetes mellitus; systemic lupus erythematosus;
KW hypertension; hypothyroidism; cholesterol ester storage disease;
KW immune deficiency; immune disorder; infectious disease;
KW autoimmune disorder; rheumatoid arthritis; autoimmune thyroiditis;
KW myasthenia gravis; gene; ss.
XX
OS Homo sapiens.
XX
XX WO200192523-A2.
XX
XX 06-DEC-2001.
XX
XX 29-MAY-2001; 2001WO-US010836.
XX
XX 30-MAY-2000; 2000US-0206132P.
XX
XX 29-AUG-2000; 2000US-0228716P.
XX
XX (CURA-) CURAGEN CORP.
XX
XX Shimkets RA, Leach MD;
XX
XX WPI; 2002-106308/14.
XX
XX P-PSDB; ABP06592.
XX
XX Novel human polypeptides and polynucleotides useful for diagnosing,
XX preventing and treating cardiovascular disease, neurodegenerative,
XX hyperproliferative disorders and autoimmune disorders.
XX
XX Disclosure; SEQ ID NO 13165; 1037pp; English.
XX
XX The present invention describes substantially purified human proteins
XX (referred to as open reading frame, ORFX, where X is 1-11491 (see Table 1
XX in the specification). ABN15762 to ABN27252 encode the human ORFX
XX proteins given in ABP00010 to ABP11500. ORFX proteins are useful for
XX treating or preventing a pathology associated with an ORFX-associated
XX disorder in humans, and in the manufacture of a medicament for treating a
XX syndrome associated with ORFX-associated disorder. ORFX polynucleotide
XX sequences can be used in gene therapy. ORFX sequences can be used in the
XX treatment of cancer, hyperproliferative disorders, cirrhosis of liver,
XX psoriasis, benign tumours, keloid, degenerative disorders, haemorrhage,
XX osteoarthritis, neurodegenerative diseases, diabetes mellitus, systemic
XX transplantation, cardiovascular diseases, hypothyroidism, cholesterol ester
XX storage disease, various immune deficiencies and disorders, infectious
XX diseases, autoimmune disorders such as multiple sclerosis, rheumatoid
XX arthritis, autoimmune thyroiditis, myasthenia gravis, graft-versus-host
XX disease and autoimmune inflammatory eye disease. ORFX proteins are also
XX useful for treating burns, incisions, ulcers, for treating osteoporosis,
XX bone degenerative disorders, or periodontal disease, and for gut
XX protection or regeneration and treatment of lung or liver fibrosis,
XX reperfusion injury in various tissues and conditions resulting from
XX systemic cytokine damage. N.B. The sequence data for this patent did not
XX form part of the printed specification, but was obtained in electronic
XX format directly from WIPO at ftp.wipo.int/pub/published_pct_sequences
XX
SQ Sequence 306 BP; 76 A; 84 C; 56 G; 88 T; 0 U; 2 Other;
Query Match 80.3%; Score 127.6; DB 6; Length 306;
Best Local Similarity 87.4%; Pred. No. 4.6e-29;
Matches 139; Conservative 0; Mismatches 20; Indels 0; Gaps 0;
QY 1 ATGGAGAAAGTCCAATACCTCACTCGCTCAGCTATAAGAGAGCCCTCAACCAATTGAAATG 60
DB 127 ATGGAAAAAGTGCATAATACCTCACTCGCTCGGTATCAGGAGAGCCCTCACTTGAATG 186
QY 61 CCTCAACAAGCAGCTCAAAAGCTACAGATCTATTATCAATTTCTGCTCATCTTAATA 120
DB 187 CCTCAGCAAGCAGCTCAGAACTCTCAGAACCTTATTAATCAATTTCTGCTCATCTTGA 246
QY 121 TGTCTCTTGTGATCTGTATCATCGTGTGATGCTTCTCTGA 159
DB 247 TGTCTCTTGTGATCTGTATCATCGTGTGATGCTTCTCTGA 285

XX PS Disclosure; Fig 7; 87pp; English.

CC The patent discloses the use of KDEL receptor inhibitor to promote

CC secretion of proteins that are normally retained within the cell such as

CC heat shock proteins by inhibiting KDEL receptor-mediated return of

CC protein complexes to endoplasmic reticulum. This makes the secreted heat

CC shock proteins more accessible to the immune system and improves immune

CC response to a target antigen. The inhibitor protein comprises several

CC subunits where each subunit comprises an oligomerisation domain and has

CC at its carboxy terminus a region which binds to a KDEL receptor. The

CC target antigen may be associated with diseases including neoplasia such

CC as sarcoma, lymphoma, leukemia, melanoma, carcinoma, glioblastoma and

CC astrocytoma, with defective tumour suppressor genes, oncogenes,

CC infectious diseases, allergy or autoimmune diseases. The present sequence

CC encodes KDEL receptor inhibitor comprising regions encoding a cleavable

CC signal peptide; the oligomerisation domain of human phospholamban (PLB)

CC pentamerisation domain; a camel IgG linker domain and the carboxy-

CC terminal sequence KDEL. The subsequence GDCC is an alteration of rat

CC cartilage oligomeric matrix protein which provides increased stability

CC via disulphide bonds. (Updated on 15-SEP-2003 to standardise OS field)

XX SQ Sequence 312 BP; 80 A; 85 C; 77 G; 70 T; 0 U; 0 Other;

Query Match 52.2%; Score 83; DB 3; Length 312;

Best Local Similarity 100.0%; Pred. No. 2.2e-15;

Matches 83; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 74 GTCAAAAGCTACAGATCTATTATCAATTTCTGCTCATCTTAATATGCTCTTGCTGA 133

DB 95 GTCAAGAGCTACAGATCTATTATCAATTTCTGCTCATCTTAATATGCTCTTGCTGA 154

QY 134 TCTGTATCATCGTGATGCTTCTC 156

DB 155 TCTGTATCATCGTGATGCTTCTC 177

RESULT 18

ADSI18082

ID ADS18082 standard; DNA; 108 BP.

XX AC ADS18082;

XX DT 30-DEC-2004 (first entry)

XX DE Human/mouse phospholamban transmembrane domain mutant, sense DNA.

XX KW Human; mouse; phospholamban; transmembrane domain; SRL;

XX KW SR localisation signal; sarco(endo)plasmic reticulum; mutant; SERCA;

XX KW sarco(endo)plasmic reticulum calcium ATPase; ss.

XX OS Homo sapiens.

XX OS Mus musculus.

XX OS Synthetic.

XX PH Key Location/Qualifiers

FT CDS 19..107

FT /*tag= a

FT /product= "Mutated phospholamban transmembrane domain"

XX PN US2004203027-A1.

XX PD 14-OCT-2004.

XX PF 29-NOV-2003; 2003US-00724532.

XX PR 02-DEC-2002; 2002US-0430322P.

XX PA (REED/) REED T D.

XX PI Reed TD;

XX WPI; 2004-728006/71.

DR P-PSDB; ADS18081.

XX PT New polypeptide sequence comprising an amino acid substitution, useful as

PT a localisation signal to target therapeutic and experimental compounds or

PT macromolecules to the sarco(endo)plasmic reticulum (SR) or eukaryotic

XX cells.

XX PS Claim 15; SEQ ID NO 3; 12pp; English.

XX CC The invention relates to a polypeptide sequence comprising ADS18080 (the

CC transmembrane domain of human/mouse phospholamban) with at least one

CC amino acid substitution at a location selected from L31, N34, F34, I38,

CC L42, V49, or L52. Also included is a nucleic acid encoding the above

CC peptide (appearing as ADS18082-ADS18085). The polypeptide is linked to a

CC compound and/or macromolecule targeted to a sarco(endo)plasmic region of

CC a cell. The polypeptide can be used as a localisation signal to target

CC therapeutic and experimental compounds or macromolecules to the

CC sarco(endo)plasmic reticulum (SR) or eukaryotic cells. The present

CC sequence encodes a mutated transmembrane domain of human/mouse

CC phospholamban which may be used as an SRL but is immune to

CC localisation signal). The peptide acts as an SRL but is immune to

CC inhibition by sarco(endo)plasmic reticulum calcium ATPase (SERCA).

XX SQ Sequence 108 BP; 21 A; 29 C; 23 G; 35 T; 0 U; 0 Other;

Query Match 28.9%; Score 46; DB 13; Length 108;

Best Local Similarity 65.7%; Pred. No. 0.00034;

Matches 67; Conservative 0; Mismatches 35; Indels 0; Gaps 0;

QY 54 TGAATGCCCTCAACAGCAGCTCAAAAGCTACAGATCTATTATCAATTTCTGCTCAT 113

DB 6 TGAGAGAAGGCCTCAGGCCAGGAGAACCTCCAGATGCTTTCATGCTTTTCTGCTGAT 65

QY 114 CTTAATATGCTCTTGTGCTGATCTGTATCATCTGATGCTTCT 155

DB 66 TCTCATCTGCTCTCTGCTGATTTGCATTATGCTCATGCTCTCT 107

RESULT 19

ADSI18083/c

ID ADS18083 standard; DNA; 108 BP.

XX AC ADS18083;

XX DT 30-DEC-2004 (first entry)

XX DE Human/mouse phospholamban transmembrane domain mutant, antisense DNA.

XX KW Human; mouse; phospholamban; transmembrane domain; SRL;

XX KW SR localisation signal; sarco(endo)plasmic reticulum; mutant; SERCA;

XX KW sarco(endo)plasmic reticulum calcium ATPase; ss.

XX OS Homo sapiens.

XX OS Mus musculus.

XX OS Synthetic.

XX PN US2004203027-A1.

XX PD 14-OCT-2004.

XX PF 29-NOV-2003; 2003US-00724532.

XX PR 02-DEC-2002; 2002US-0430322P.

XX PA (REED/) REED T D.

XX PI Reed TD;

XX WPI; 2004-728006/71.

XX PT New polypeptide sequence comprising an amino acid substitution, useful as

PT a localisation signal to target therapeutic and experimental compounds or

PT macromolecules to the sarco(endo)plasmic reticulum (SR) or eukaryotic

ID	AAV46494	standard; cDNA; 2071 BP.	
XX	AAV46494;		
XX	11-JAN-1999	(first entry)	
XX	Interleukin-1	beta converting enzyme apoptosis protease-10 cDNA.	
XX	Interleukin-1	beta converting enzyme apoptosis protease-10; ICE-LAP-10; human; cancer; inflammation; autoimmunity; allergy; asthma; rheumatoid arthritis; cerebellar degeneration; Alzheimer's disease; Parkinson's disease; multiple sclerosis; amyotrophic lateral sclerosis; head injury; septic shock; sepsis; stroke; osteoporosis; osteoarthritis; ischaemia; kidney disease; reperfusion injury; cardiovascular disease; liver disease; myocardial infarction; hypotension; hypertension; AIDS; myelodysplastic syndrome; aplastic anaemia; male pattern baldness; infection; therapy; diagnosis; ss.	
XX	Homo sapiens.		
XX	Key	Location/Qualifiers	
XX	FT	73..1206	
XX	FT	/*tag= a	
XX	EP867513-A2.		
XX	30-SEP-1998.		
XX	23-MAR-1998;	98EP-00302150.	
XX	27-MAR-1997;	97US-0042030P.	
XX	(SMIK)	SMITHKLINE BEECHAM CORP.	
XX	Kikly KK;		
XX	WPI; 1998-497864/43.		
XX	P-PSDB; AAV76330.		
XX	New ICE-LAP 10	polypeptide and polynucleotide - used for treatment of e.g. cancer, inflammation, allergy, asthma, rheumatoid arthritis, stroke and ischaemia.	
XX	Claim 2vi;	Page 15-16; 19pp; English.	
XX	This nucleotide	sequence codes for human interleukin-1 beta converting enzyme apoptosis protease-10 (ICE-LAP-10, see AAV76330) that is structurally related to the ICE/ced-3 or caspase-3 family of cysteine proteases. ICE-LAP-10 polynucleotides may be obtained using standard cloning and screening techniques, from a human skin fibroblast cDNA using EST analysis, or from natural sources such as genomic DNA libraries. The ICE-LAP-10 polypeptides and polynucleotides can be used in the treatment and diagnosis of cancer, inflammation, autoimmunity, allergy, asthma, rheumatoid arthritis, CNS inflammation, cerebellar degeneration, Alzheimer's disease, Parkinson's disease, multiple sclerosis, amyotrophic lateral sclerosis, head injury damage, and other neurological abnormalities, septic shock, sepsis, stroke, osteoporosis, osteoarthritis, ischaemia, reperfusion injury, cardiovascular disease, kidney disease, liver disease, ischemic injury, myocardial infarction, hypotension, hypertension, AIDS, myelodysplastic syndromes and other haematologic abnormalities, aplastic anaemia, male pattern baldness, and bacterial, fungal, protozoal and viral infections. The polynucleotides may be used as hybridisation probes for cDNA and genomic DNA, as PCR primers, as diagnostic reagents, for chromosome identification, and for recombinant production of ICE-LAP-10	
XX	Sequence 2071 BP;	673 A; 399 C; 434 G; 565 T; 0 U; 0 Other;	
XX	Query Match	21.8%; Score 34.6; DB 2; Length 2071;	
XX	Best Local Similarity	58.1%; Pred. No. 2.6;	
XX	Matches	61; Conservative 0; Mismatches 44; Indels 0; Gaps 0;	
Qy	34	ATAGAGAGCGCTCAACCATTTGAAATGCTCAACAAGCAGCTCAACAGCTACAGAATCTA 93	
Db	1215	ATCAGGAAATTCACCAATTTATCAGCTTCAGAGCATTTTATCAGCAGCATCCA 1274	
Qy	94	TTTATCAATTTCTGCTCATCTTAATATGTCCTCTTGTGATCTGT 138	
Db	1275	TGTTTAACTTTTGCTTTTCATTAAAGTGAAAACATATGAACCTGT 1319	
RESULT 25			
ABL34196/c			
ID	ABL34196	standard; DNA; 37973 BP.	
XX	ABL34196;		
XX	26-MAR-2002	(first entry)	
XX	Human immune	system associated gene SEQ ID NO: 2169.	
XX	Human; immune	system disease; cytosine methylation; antiasthmatic; antiarteriosclerotic; antianaemic; cytosolic; neutropenic; neuroprotective; anti-HIV; anticonvulsant; ophthalmological; antiinflammatory; antiarthritic; antidiabetic; antipsoriatic; antiinflammatory; cancer; eye disease; arteriosclerosis; anaemia; acute myeloid leukaemia; Alzheimer's disease; AIDS; epilepsy; neurofibromatosis; rheumatoid arthritis; psoriasis; bowel disease; gene; ds.	
XX	Homo sapiens.		
XX	WO200200928-A2.		
XX	03-JAN-2002.		
XX	02-JUL-2001;	2001WO-EP007537.	
XX	30-JUN-2000;	2000DE-01032529.	
XX	01-SEP-2000;	2000DE-01043826.	
XX	(EPIG-)	EPIGENOMICS AG.	
XX	Olek A,	Piepenbrock C, Berlin K;	
XX	WPI; 2002-130909/17.		
XX	Nucleic acid	comprising fragment of chemically modified gene, useful for diagnosis and treatment of diseases associated with abnormal cytosine methylation.	
XX	Claim 1;	SEQ ID NO 2169; 32pp + Sequence Listing; German.	
XX	The present	invention provides a number of human immune system associated genes which are modified by the methylation of cytosines. The sequences can be used in the diagnosis and treatment of immune system disorders, including eye diseases such as retinopathy, neovascular glaucoma and macular degeneration, arteriosclerosis, anaemia, cancer, acute myeloid leukaemia, Alzheimer's disease, AIDS, epilepsy, neurofibromatosis, rheumatoid arthritis, psoriasis and inflammatory/ulcerative bowel diseases. The present sequence is a gene of the invention	
XX	Sequence 37973 BP;	10166 A; 620 C; 8741 G; 18446 T; 0 U; 0 Other;	
XX	Query Match	21.0%; Score 33.4; DB 6; Length 37973;	
XX	Best Local Similarity	62.7%; Pred. No. 15;	
XX	Matches	52; Conservative 0; Mismatches 31; Indels 0; Gaps 0;	
Qy	72	ACGTCAAAGCTACAGAAATCTATTATCAATTTCTGCTCATCTTAATATGTCCTTGTCT 131	
Db	12130	ACTTCCACATTTATAAATATATTATCTATATATTTCTTTCTTATAATATCTTCTCT 12071	
Qy	132	GATCTGTATCATCTGATGCTTC 154	
Db	12070	AATTTTAAACAACAATAATATAC 12048	

XX
SQ Sequence 80268 BP; 21229 A; 17453 C; 18157 G; 22885 T; 0 U; 544 Other;
Query Match 20.9%; Score 33.2; DB 13; Length 80268;
Best Local Similarity 71.0%; Pred. No. 21;
Matches 44; Conservative 0; Mismatches 18; Indels 0; Gaps -0;
QY 83 TACAGAATCTATTATCAATTTCTGTCATCTTAATATGTCCTCTGTCGATCTGATCA 142
DB 37830 TACAGATGTAGTCATCAAAATCTATTACATCTATATATTTCTAGTGCCCATCTTTTCC 37771
QY 143 TC 144
DB 37770 TC 37769
RESULT 27
ABD32686/c
ID ABD32686 standard; DNA; 170279 BP.
XX AC ABD32686;
XX 18-NOV-2004 (first entry)
XX Mouse cancer-associated genomic DNA MD14-005.
XX Mouse; ds; cancer-associated protein; gene; cytostatic; cancer;
XX leukaemia; lymphoma; CAP.
XX Mus musculus.
XX WO2004074320-A2.
XX 02-SEP-2004.
XX 17-FEB-2004; 2004WO-US004730.
XX 14-FEB-2003; 2003US-00367094.
XX 14-MAR-2003; 2003US-00388838.
XX 15-APR-2003; 2003US-00417375.
XX 13-JUN-2003; 2003US-00461862.
XX 15-SEP-2003; 2003US-00663431.
XX 15-DEC-2003; 2003US-00737318.
XX (SAGR-) SAGRES DISCOVERY INC.
XX Morris DW, Morris DW, Malandro MS;
XX WPI; 2004-652914/63.
XX New isolated cancer-associated polynucleotides and polypeptides useful
XX for diagnosing, preventing or treating cancers, especially lymphoma and
XX leukemia, or in screening for agents that modulate cancer.
XX disclosure; seqid 242; 310pp; English.
XX The invention relates to an isolated nucleic acid comprising at least 10
XX contiguous nucleotides of any of the 233 polynucleotide sequences given
XX in the specification, or its complement. The nucleic acids encode cancer-
XX associated proteins. Also included are an expression vector comprising
XX the isolated nucleic acid cited above, a host cell comprising the above
XX recombinant nucleic acid or expression vector, a microarray for detecting
XX a cancer-associated (CA) nucleic acid comprising at least one probe
XX comprising at least 10 contiguous nucleotides of any of the above-
XX mentioned nucleotide sequences, an isolated polypeptide (encoded within
XX an open reading frame of a CA sequence selected from any of the 95
XX polynucleotide sequences as mentioned in the specification, or its
XX complement), an isolated antibody, (or its antigen binding fragment) that
XX binds to the above polypeptide, a hybridoma that produces the above
XX monoclonal antibody, a pharmaceutical composition comprising the above
XX antibody and a pharmaceutical excipient, a kit for detecting cancer
XX cells (comprising the antibody cited above, methods for diagnosing cancer
XX or for detecting the presence or absence of cancer cells in an

RESULT 26
ABD32951/c
ID ABD32951 standard; DNA; 80268 BP.
XX AC ABD32951;
XX 18-NOV-2004 (first entry)
XX Mouse cancer-associated genomic DNA MD20-011.
XX Mouse; ds; cancer-associated protein; gene; cytostatic; cancer;
XX leukaemia; lymphoma; CAP.
XX Mus musculus.
XX WO2004074320-A2.
XX 02-SEP-2004.
XX 17-FEB-2004; 2004WO-US004730.
XX 14-FEB-2003; 2003US-00367094.
XX 14-MAR-2003; 2003US-00388838.
XX 15-APR-2003; 2003US-00417375.
XX 13-JUN-2003; 2003US-00461862.
XX 15-SEP-2003; 2003US-00663431.
XX 15-DEC-2003; 2003US-00737318.
XX (SAGR-) SAGRES DISCOVERY INC.
XX Morris DW, Morris DW, Malandro MS;
XX WPI; 2004-652914/63.
XX New isolated cancer-associated polynucleotides and polypeptides useful
XX for diagnosing, preventing or treating cancers, especially lymphoma and
XX leukemia, or in screening for agents that modulate cancer.
XX disclosure; seqid 685; 310pp; English.
XX The invention relates to an isolated nucleic acid comprising at least 10
XX contiguous nucleotides of any of the 233 polynucleotide sequences given
XX in the specification, or its complement. The nucleic acids encode cancer-
XX associated proteins. Also included are an expression vector comprising
XX the isolated nucleic acid cited above, a host cell comprising the above
XX recombinant nucleic acid or expression vector, a microarray for detecting
XX a cancer-associated (CA) nucleic acid comprising at least one probe
XX comprising at least 10 contiguous nucleotides of any of the above-
XX mentioned nucleotide sequences, an isolated polypeptide (encoded within
XX an open reading frame of a CA sequence selected from any of the 95
XX polynucleotide sequences as mentioned in the specification, or its
XX complement), an isolated antibody, (or its antigen binding fragment) that
XX binds to the above polypeptide, a hybridoma that produces the above
XX monoclonal antibody, a pharmaceutical composition comprising the above
XX antibody and a pharmaceutical excipient, a kit for detecting cancer
XX cells (comprising the antibody cited above, methods for diagnosing cancer
XX or for detecting the presence or absence of cancer cells in an
XX individual, a method for inhibiting growth of cancer cells in an
XX individual, a method for delivering a therapeutic agent to cancer cells
XX in an individual, an electronic library comprising the above
XX polynucleotide or polypeptide (or their fragments), methods of screening
XX for anticancer activity or for a bioactive agent capable of modulating
XX the activity of a CA protein (CAP), methods for detecting cancer
XX associated with expression of a polypeptide in a test cell sample, a
XX method for treating cancers and a method for inhibiting the expression of
XX a CA gene in a cell. The composition and methods are useful for detecting,
XX diagnosing, preventing and treating cancers, especially lymphoma and
XX leukaemia. These may also be used in screening for agents that modulate
XX cancer. The present sequence is a mouse CAP genomic sequence. Note: The
XX sequence data for this patent did not form part of the printed
XX specification, but was obtained in electronic format directly from WIPO
XX at ftp.wipo.int/pub/published_pct_sequences

CC individual, a method for inhibiting growth of cancer cells in an
CC individual, a method for delivering a therapeutic agent to cancer cells
CC in an individual, an electronic library comprising the above
CC polynucleotide or polypeptide (or their fragments), methods of screening
CC for anticancer activity or for a bioactive agent capable of modulating
CC the activity of a CA protein (CAP), methods for detecting cancer
CC associated with expression of a polypeptide in a test cell sample, a
CC method for treating cancers and a method for inhibiting the expression of
CC CA gene in a cell. The composition and methods are useful for detecting,
CC diagnosing, preventing and treating cancers, especially lymphoma and
CC leukaemia. These may also be used in screening for agents that modulate
CC cancer. The present sequence is a mouse CAP genomic sequence. Note: The
CC sequence data for this patent did not form part of the printed
CC specification, but was obtained in electronic format directly from WIPO
CC at ftp.wipo.int/pub/published_pct_sequences
XX
SQ Sequence 170279 BP; 51527 A; 31503 C; 31927 G; 54249 T; 0 U; 1073 Other;

Query Match 20.5%; Score 32.6; DB 13; Length 170279;
Best Local Similarity 51.7%; Pred. No. 41;
Matches 74; Conservative 0; Mismatches 69; Indels 0; Gaps 0;

QY 15 ATACCTCACTCGCTCAGCTATAGAGAGCGCTCAACCAATTGAATGCTCAACAGCAGC 74
DB 142522 AAAGCTCAGCTCTTTGGTTATGATATAGCTCAGTTCTTGCATGACTAACTGATCACA 142463
QY 75 TCAAAAGCTACAGATCTATTTATCAATTTCTCTCATCTTAATATGCTCTTGTGAT 134
DB 142462 GAATAGCTGCAGTATATATGCAACACTTAATTTGTTTCATGCTGTTCACTGCCCT 142403
QY 135 CTGTATCATCGTGATGCTTCTCT 157
DB 142402 TTATTTCTATTGTTTGACCTCT 142380

RESULT 28
AAQ64111/C
ID AAQ64111 standard; DNA; 3713 BP.
XX
AC AAQ64111;
XX
DT 02-FEB-1995 (first entry)
XX
DE cryET4 gene.
XX
KW cryET4; cryET5; Lepidoptera; lepidopteran insect; insecticidal; toxin;
KW insecticidal crystal protein; ICP; ds.
XX
OS Bacillus thuringiensis.
XX
FH Key Location/Qualifiers
FT CDS 99..3602
FT /*tag= a
FT /note= "claim 2"
XX
PN US5322687-A.
XX
XX 21-JUN-1994.
XX
XX 29-JUL-1993; 93US-00100709.
XX
XX 29-JUL-1993; 93US-00100709.
XX
XX (ECOG-) ECOGEN INC.
XX
XX Tan Y, Jany CS, Donovan WP, Gonzalez JM;
XX
XX WPI; 1994-199503/24.
XX P-PSDB; AAR54073.
XX
XX Isolated cryET4 gene and Bacillus thuringiensis cultures transformed with
XX this gene - used in compsns. against lepidopteran insects.
XX
XX

PS Claim 2; Col 15-24; 51pp; English.
XX
CC B. thuringiensis strain EG5847 exhibits insecticidal activity against
CC lepidopteran insects. Two novel toxin genes from B. thuringiensis EG5847
CC designated cryET4 and cryET5 produce insecticidal proteins with activity
CC against a broad spectrum of lepidopteran insects. The gene sequences are
CC given in AAQ64111-12
XX
SQ Sequence 3713 BP; 1253 A; 609 C; 802 G; 1049 T; 0 U; 0 Other;

Query Match 20.3%; Score 32.2; DB 2; Length 3713;
Best Local Similarity 61.2%; Pred. No. 17;
Matches 52; Conservative 0; Mismatches 33; Indels 0; Gaps 0;

QY 73 CGTCAAAAGCTACAGATCTATTTATCAATTTCTGCTCACTTAATATGCTCTTGTG 132
DB 441 CTTTAAATGCTTCAGCGTATATTTGATAATTTCTCCCTAATCCCTCTAATCAGTATG 382
QY 133 ATCTGTATCATCGTGATGCTTCTCT 157
DB 381 CTTTGTCTTACTGTTGCTTCTAT 357

RESULT 29
AAT95050/C
ID AAT95050 standard; DNA; 3713 BP.
XX
AC AAT95050;
XX
DT 17-FEB-1998 (first entry)
XX
DE DNA encoding Bacillus thuringiensis crystal toxin cryET4.
XX
KW EG7279; crystal toxin; cryET4; lepidopteran pest; Heliothis virescens;
KW Helicoverpa zea; Lymantria dispar; Ostrinia nubilalis;
KW Pseudoplusia includens; Plutella xylostella; Spodoptera exigua;
KW Spodoptera frugiperda; Trichoplusia ni; ds.
XX
OS Bacillus thuringiensis.
XX
FH Key Location/Qualifiers
FT CDS 99..3602
FT /*tag= a
FT /product= "CryET4"
XX
PN US5679343-A.
XX
XX 21-OCT-1997.
XX
XX 07-JUN-1995; 95US-00474038.
XX
XX 29-JUL-1993; 93US-00100709.
XX 30-DEC-1993; 93US-00176865.
XX
XX (MONS) MONSANTO CO.
XX
XX Jany CS, Gonzalez JM, Donovan WP, Tan Y;
XX
XX WPI; 1997-525682/48.
XX P-PSDB; AAW35250.
XX
XX Lepidopteran toxic Bacillus thuringiensis crystal protein - useful to
XX control Lepidopteran pests.
XX
XX Example 2; Col 15-24; 50pp; English.
XX
XX The present sequence encodes the Bacillus thuringiensis EG7279 crystal
XX toxin cryET4, which, optionally in association with B. thuringiensis
XX EG7279, can be used against lepidopteran pests. cryET4 is especially
XX useful for controlling Heliothis virescens, Helicoverpa zea, Lymantria
XX dispar, Ostrinia nubilalis, Pseudoplusia includens, Plutella xylostella,
XX Spodoptera exigua, Spodoptera frugiperda and Trichoplusia ni
XX
XX

Sequence	3713 BP; 1254 A; 609 C; 802 G; 1048 T; 0 U; 0 Other;
Query Match	20.3%; Score 32.2; DB 2; Length 3713;
Best Local Similarity	61.2%; Pred. No. 17;
Matches	52; Conservative 0; Mismatches 33; Indels 0; Gaps 0;
QY	73 CGTCAAAAGCTACAGAACTATTATTCATCAATTTCTGCTCATCTTAATATGCTCTTCTGCTG 132
DB	441 CTTTAAATGCTTCAGGTATATTTCATTAATTTCTCCCTAACTCTTAATTCAGTGATTG 382
QY	133 ATCTGTATCAATCGTGATGCTTCTCT 157
DB	381 CTTTGGCTCTTACTGTTGCTTCTAT 357
RESULT 30	
AAT68435/c	
ID	AAT68435 standard; DNA; 3713 BP.
XX	
AC	AAT68435;
XX	
DT	25-MAR-2003 (revised)
DT	07-JUL-1997 (first entry)
XX	
DE	CryET4 gene.
XX	
KW	CryET5; cryET4; Bacillus thuringiensis; insecticidal crystal protein;
KW	ICP; toxin; CryI protein; lepidopteran insect; insecticide; ds.
XX	
OS	Bacillus thuringiensis.
XX	
FH	Key Location/Qualifiers
FT	CDS 99..3602
FT	/*tag= a
FT	/product= "cryET4"
XX	
FN	US5616319-A.
XX	
PD	01-APR-1997.
XX	
PF	30-DEC-1993; 93US-00176865.
XX	
PR	29-JUL-1993; 93US-00100709.
XX	
PA	(MONS) MONGANTO CO.
XX	
PI	Gonzalez JM, Donovan WP, Tan Y, Jany CS;
XX	
DR	WPI; 1997-212077/19.
DR	P-PSDB; AAW17700.
XX	
PT	Bacillus thuringiensis cryET5 gene encoding insecticidal protein - useful
PT	for control of lepidopteran pests.
XX	
PS	Example 3; Col 15-24; 50pp; English.
XX	
CC	This sequence represents the cryET4 gene of Bacillus thuringiensis (B.t.)
CC	isolate EG5847. B.t. produces inclusions during sporulation which include
CC	insecticidal crystal proteins (ICP). ICP toxins are active in insects
CC	only after ingestion. Once ingested, the toxic components disrupt the
CC	midgut cells, resulting in cessation of feeding, and eventually death.
CC	The CryI proteins produced by B.t. are active against lepidopteran
CC	insects. The protein encoded by this sequence, and the CryET5 protein
CC	(see AAW17699) belong to the CryI family of ICPs. This sequence can be
CC	used to transform bacteria, which are useful as insecticides against a
CC	wide range of lepidopteran pests, and can be applied to crops, soil and
CC	seeds. The encoded protein, or especially its toxic N terminal region,
CC	can be expressed in plants, to provide protection against lepidopteran
CC	pests. This sequence, or its fragments, can also be used to isolate other
CC	similar genes. (Updated on 25-MAR-2003 to correct PF field.)
XX	
SQ	Sequence 3713 BP; 1254 A; 609 C; 802 G; 1048 T; 0 U; 0 Other;

Db 441 CTTTAAATGCTTCAGCGTATATTTGATAATTTCTCCCTAAATGCTTCTTAATTCAGTGATTG 382

Qy 133 ATCTGTATCATCGTGCATGCTTCTCT 157

Db 381 CTTTGTCTTACTGTGCTTCTAT 357

RESULT 32
AAZ09159/c
ID AAZ09159 standard; DNA; 3713 BP.
XX
AC AAZ09159;
XX
DT 18-OCT-1999 (first entry)
XX
DE B. thuringiensis cryET4 toxin DNA.
XX
KW Toxin; cryET4; cryET5; insecticidal; Lepidoptera; transformed plant;
KW crystal protein; insect; ds.
XX
OS Bacillus thuringiensis.
XX
FH Key Location/Qualifiers
FT CDS 99..3602
FT /*tag a
FT /product= "cryET4"
XX
XX US5942658-A.
XX
XX 24-AUG-1999.
XX
XX 24-JUN-1997; 97US-00881340.
XX
XX 29-JUL-1993; 93US-00100709.
XX 30-DEC-1993; 93US-00176865.
XX 07-JUN-1995; 95US-00474038.
XX
XX (MONS) MONSANTO CO.
XX
XX Gonzalez JM, Jany CS, Tan Y, Donovan WP;
XX
XX WPI; 1999-493544/41.
XX P-PSDB; AAY30922.
XX
XX Transformed plant comprising insecticidal crystal proteins.
XX
XX Claim 2; Fig 1A-J; 50pp; English.
XX
XX This invention describes novel transformed plants containing Bacillus
CC thuringiensis strain BG5847 insecticidal crystal protein genes cryET4 or
CC cryET5. cryET4 and cryET5 are novel toxin genes which produce
CC insecticidal proteins with activity against a broad spectrum of insects
CC of the order Lepidoptera. This sequence encodes the cryET4 protein
CC described in the method of the invention
XX
XX Sequence 3713 BP; 1254 A; 609 C; 802 G; 1048 T; 0 U; 0 Other;
SQ
Query Match 20.3%; Score 32.2; DB 2; Length 3713;
Best Local Similarity 61.2%; Pred. No. 17;
Matches 52; Conservative 0; Mismatches 33; Indels 0; Gaps 0;
Qy 73 CGTCAAAAGCTACAGATCTATTTATCAATTTCTGCTCATCTTAATATGCTTCTGCTG 132
Db 441 CTTTAAATGCTTCAGCGTATATTTGATAATTTCTCCCTAAATGCTTCTTAATTCAGTGATTG 382

Qy 133 ATCTGTATCATCGTGCATGCTTCTCT 157

Db 381 CTTTGTCTTACTGTGCTTCTAT 357

RESULT 33
ADO43653/c

ID ADO43653 standard; DNA; 127432 BP.
XX
AC ADO43653;
XX
DT 29-JUL-2004 (first entry)
XX
DE Nucleotide sequence of BAC-64.
XX
KW pentatricopeptide sequence; PPR sequence; ppr-A; ppr-B; ppr-C;
KW male fertility; plant; Rfo locus; radish; Brassica; cytoplasmic inducer;
KW BAC; primer; ss.
XX
OS Synthetic.
XX
PN WO2004039988-A1.
XX
PD 13-MAY-2004.
XX
PF 29-OCT-2003; 2003WO-FR003224.
XX
PR 29-OCT-2002; 2002FR-00013512.
XX
XX (GENO-) GENOPLANTE-VALOR.
XX
XX Budar F, Giancola S, Bendahmane A, Desloire S, Delourme R;
PI Marhadour S, Falentin-Guyomarc'h H, Falentin C, Renard M, Gherbi H;
PI Laloui W, Bonden S, Wilmer J, Clouet V;
XX
DR WPI; 2004-376197/35.
XX
XX New pentatricopeptides from plants, useful for restoration of male
PT fertility in Brassica containing cytoplasmic inducer of male sterility,
PT especially for production of colza hybrids, also related nucleic acids.
XX
XX Example 1; Page 67-102; 106pp; French.
XX
XX The present sequence represents bacterial artificial chromosome (BAC)-64.
CC This BAC contains the Rfo locus, which contains pentatricopeptide (PPR)
CC sequences. The specification describes PPR sequences, designated ppr-A,
CC ppr-B and ppr-C. These PPR sequences are able to restore male fertility
CC in plant. PPR sequences, used singly or in combination, are used to
CC restore male fertility in Brassica, specifically B. napus, that contain a
CC cytoplasmic inducer of male sterility. The plants with restored fertility
CC are used for production of hybrids.
XX
SQ Sequence 127432 BP; 42300 A; 21940 C; 21537 G; 40004 T; 0 U; 1651 Other;
Query Match 20.3%; Score 32.2; DB 12; Length 127432;
Best Local Similarity 50.3%; Pred. No. 50;
Matches 76; Conservative 0; Mismatches 75; Indels 0; Gaps 0;
Qy 7 AAGTCCAAATACCTCACTCGCTCAGCTATAAGAGAGCGCTCAACCATTTGAATGCCTCAA 66
Db 13865 AAGTCNAGAAGCATATATCTCCGTTTCAAAATCCAGCTTCAATAATACATCTGAGA 13806
Qy 67 CAAGCAGCTCAAAAGCTACAGAACTATTTATCAATTTCTGCTCATCTTAATATGCTC 126
Db 13805 AAGTACCTCCACTTTTCTTAGCTTACATTCGCTCAATTTCTTCTTCTTAATCAGTTT 13746
Qy 127 TTGCTGATCTGTATCATCGTGATGCTTCTCT 157
Db 13745 CATAGANGCAGTGTGCTGCAAACTCTTCTTCT 13715
RESULT 34
ADN73394/c
ID ADN73394 standard; cDNA; 1590 BP.
XX
AC ADN73394;
XX
DT 15-JUL-2004 (first entry)
XX
DE Thale cress cDNA upregulated in E2Pa/Dpa expressing plants SeqID 1289.

XX KW gene; ss; plant; transgenic; E2Fa/Dpa transcription factor;
XX KW growth regulator; animal feed product; thale cress;
XX KW cell wall biosynthesis; nitrogen metabolism; carbon metabolism.
XX OS Arabidopsis thaliana.
XX PN WO2004035798-A2.
XX XX 29-APR-2004.
XX XX 20-OCT-2003; 2003WO-EP011658.
XX PF 18-OCT-2002; 2002EP-00079408.
XX XX (CROP-) CROPDISEIGN NV.
XX PI Inze D, De Veylder L, Vlieghe K;
XX XX WPI; 2004-348466/32.
XX DR P-PSDB; ADN73395.
XX XX
XX PT Altering plant characteristics, useful for producing plants for enzyme or
XX PT pharmaceutical production comprises modifying in a plant, expression of
XX PT one or more nucleic acids and/or modifying level or activity of one or
XX PT more proteins.
XX PS Claim 1; SEQ ID NO 1289; 134pp; English.
XX XX
XX CC This invention relates to a novel method for altering one or more plant
XX CC characteristics. Specifically, it refers to identifying genes that are up
XX CC - or down-regulated in transgenic plants overexpressing the heterodimeric
XX CC E2Fa/Dpa transcription factor of Arabidopsis and using these sequences to
XX CC alter plant characteristics accordingly. The present invention describes
XX CC generating transgenic plants for the production of growth regulators,
XX CC enzymes, therapeutics, pharmaceuticals and animal feed products, where
XX CC the altered plant characteristics are selected from increased yield or
XX CC biomass, enhanced survival capacity, stress tolerance, plant architecture
XX CC or physiology, altered endoreplication, biochemistry, signal
XX CC transduction, storage lipid mobilisation and/or altered photosynthesis,
XX CC each relative to the corresponding wild type plants. Accordingly, these
XX CC sequences can also be useful as positive or negative selectable markers
XX CC during transformation of cells or tissues. The identified genes play a
XX CC role in a variety of biological processes such as DNA replication, cell
XX CC wall biosynthesis, nitrogen and/or carbon metabolism or they function as
XX CC transcription factors. This polynucleotide sequence is thale cress cDNA
XX CC upregulated 1.3 fold or more in plants overexpressing the E2Fa/Dpa
XX CC transcription factor, given in an exemplification of the invention.
XX SQ Sequence 1590 BP; 440 A; 289 C; 442 G; 419 T; 0 U; 0 Other;
Query Match 20.1%; Score 32; DB 12; Length 1590;
Best Local Similarity 51.4%; Pred. No. 15;
Matches 74; Conservative 0; Mismatches 70; Indels 0; Gaps 0;
QY 13 CAATACCTCACTCGCTCAGCTAATAAGAGAGCCTCAACCAATTCGCTCAACAGCA 72
Db 1449 CAGCTCCACCGCGCTCTCATTCAGATGCTCAGAACCAATATGCCAGGATAAC 1390
QY 73 CGTCAAAAGCTACAGAACTATTATTAATTCATCTTCATCTTAATATGCTCTCTGCTG 132
Db 1389 AGCAACAAGCTGAAGACTGTAGAGACCTGATTCAGCTTCGATTAATTCATCTTC 1330
QY 133 ATCTGTATCATCTGTGATGCTTCTC 156
Db 1329 ATCCAACCTCAAGGTCAATCAAGCTC 1306
RESULT 35
ID AAV74594
XX AAV74594 standard; DNA; 1421 BP.
AC AAV74594;
XX 16-MAR-1999 (first entry)
XX Staphylococcus aureus contig SEQ ID #283.
XX Computer readable medium; vaccine; S.aureus infection; immunodetection;
XX cellulitis; eyelid infection; food poisoning; osteomyelitis; therapy;
XX skin infection; surgical wound infection; scalded skin syndrome;
XX toxic shock syndrome; ds.
XX Staphylococcus aureus.
XX Key Location/Qualifiers
XX FT 481..540
XX FT /*tag= a
XX FT the sequence listing in the specification. They are
XX FT included to maintain the nucleotide numbering given in
XX FT the specification for this DNA sequence"
XX PN EP786519-A2.
XX XX
XX PD 30-JUL-1997.
XX XX
XX PF 07-JAN-1997; 97EP-00100117.
XX PR 05-JAN-1996; 96US-0009861P.
XX XX (HUMA-) HUMAN GENOME SCI INC.
XX PA Kunsch CA, Choi GH, Barash SC, Dillon PJ, Fannon MR, Rosen CA;
XX PI WPI; 1997-374922/35.
XX DR Polynucleotide(s) and proteins derived from Staphylococcus aureus -
XX PT stored on computer readable medium and used in the production of anti-
XX PT S.aureus vaccines.
XX PS Claim 1; Page 1107-1108; 327pp; English.
XX CC This sequence represents one of 5191 Staphylococcus aureus DNA sequences
XX CC of the invention. The DNA sequences are recorded on a computer readable
XX CC medium, preferably selected from a floppy or hard disk, random access
XX CC memory (RAM), read-only memory (ROM) or CD-ROM. Homology searches using
XX CC the S.aureus DNA sequences allows putative functions to be assigned so
XX CC that protein-encoding or regulatory regions of commercial, therapeutic or
XX CC industrial importance can be obtained. Specifically, sequences which are
XX CC likely to encode antigens have been identified and these polypeptides can
XX CC be used in a vaccine composition against S.aureus infection. The
XX CC polypeptides can also be used in a kit for the immunodetection of
XX CC S.aureus in a sample. S.aureus is implicated in numerous human diseases,
XX CC including cellulitis, eyelid infections, food poisoning, osteomyelitis,
XX CC skin and surgical wound infections, scalded skin syndrome, toxic shock
XX CC syndrome, etc. Organisms transformed with the DNA sequences can be used
XX CC for recombinant production of the polypeptides. The new DNA sequences
XX CC (and their fragments) are useful as primers or probes for isolating
XX CC homologues of any of the S.aureus DNA sequences contained on the computer
XX CC readable medium
XX SQ Sequence 1421 BP; 506 A; 174 C; 258 G; 422 T; 0 U; 61 Other;
Query Match 20.0%; Score 31.8; DB 2; Length 1421;
Best Local Similarity 61.4%; Pred. No. 17;
Matches 51; Conservative 0; Mismatches 32; Indels 0; Gaps 0;
QY 36 AAGAGAGCCTCAACCAATTCGCTCAACCAAGCAGCTCAACCAAGCTACAGATCTATT 95
Db 317 ACGAAGAACTGAAATTTTGAATGGTGGTAATCATGCTCAAAATATATAGTCAAGATGA 376
QY 96 TATCAATTTCTCTCATCTTAA 118
Db 377 CTTCAATTACTCTATAAATAA 399

XX AAS69551;
AC
DT 13-FEB-2002 (first entry)
XX
DE DNA encoding novel human diagnostic protein #5355.
XX
KW Human; chromosome mapping; gene mapping; gene therapy; forensic;
KW food supplement; medical imaging; diagnostic; genetic disorder; ss.
XX Homo sapiens.
XX WO200175067-A2.
XX 11-OCT-2001.
XX 30-MAR-2001; 2001WO-US008631.
XX 31-MAR-2000; 2000US-00540217.
XX 23-AUG-2000; 2000US-00649167.
XX (HYSE-) HYSEQ INC.
XX Drmanac RT, Liu C, Tang YT;
PI P-PSDB; ABG05364.
XX WPI; 2001-639362/73.
XX P-PSDB; ABG05364.
XX New isolated polynucleotide and encoded polypeptides, useful in
XX diagnostics, forensics, gene mapping, identification of mutations
XX responsible for genetic disorders or other traits and to assess
XX biodiversity.
XX Claim 1; SEQ ID NO 5355; 103pp; English.
XX The invention relates to isolated polynucleotide (I) and polypeptide (II)
XX sequences. (I) is useful as hybridisation probes, polymerase chain
XX reaction (PCR) primers, oligomers, and for chromosome and gene mapping,
XX and in recombinant production of (II). The polynucleotides are also used
XX in diagnostics as expressed sequence tags for identifying expressed
XX genes. (I) is useful in gene therapy techniques to restore normal
XX activity of (II) or to treat disease states involving (II). (II) is
XX useful for generating antibodies against it, detecting or quantitating a
XX polypeptide in tissue, as molecular weight markers and as a food
XX supplement. (II) and its binding partners are useful for treating disorders
XX of sites expressing (II). (I) and (II) are useful for biological actions. The
XX involving aberrant protein expression or biological actions in
XX polypeptide and polynucleotide sequences have applications in
XX diagnostics, forensics, gene mapping, identification of mutations
XX and to produce other types of data and products dependent on DNA and
XX amino acid sequences. AAS64197-AAS94564 represent novel human diagnostic
XX coding sequences of the invention. Note: The sequence data for this
XX patent did not appear in the printed specification, but was obtained in
XX electronic format directly from WIPO at
XX ftp.wipo.int/pub/published_pct_sequences
XX
XX Sequence 873 BP; 235 A; 191 C; 229 G; 218 T; 0 U; 0 Other;
Query Match 19.7%; Score 31.4; DB 5; Length 873;
Best Local Similarity 53.7%; Pred. No. 19;
Matches 65; Conservative 0; Mismatches 56; Indels 0; Gaps 0;
QY 37 AGAAGAGCCTCAACCATTTGAAATGCCCTCAACAGCAGCTCAAAAGCTACAGAAATCTATTT 96
DB 207 AAAGAAACATATACCATTAATAAATTTGCATATAGGTATTAATATCTTCCCAATCATC 148
QY 97 ATCAATTTCTGTCTCATCTTTAATATGCTCTTGTGATCTGTATCATCGATGCTTCTC 156
DB 147 TTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTC 88
QY 157 T 157

XX AAS69551;
AC
DT 13-FEB-2002 (first entry)
XX
DE DNA encoding novel human diagnostic protein #5355.
XX
KW Human; chromosome mapping; gene mapping; gene therapy; forensic;
KW food supplement; medical imaging; diagnostic; genetic disorder; ss.
XX Homo sapiens.
XX WO200175067-A2.
XX 11-OCT-2001.
XX 30-MAR-2001; 2001WO-US008631.
XX 31-MAR-2000; 2000US-00540217.
XX 23-AUG-2000; 2000US-00649167.
XX (HYSE-) HYSEQ INC.
XX Drmanac RT, Liu C, Tang YT;
PI P-PSDB; ABG05364.
XX WPI; 2001-639362/73.
XX P-PSDB; ABG05364.
XX New isolated polynucleotide and encoded polypeptides, useful in
XX diagnostics, forensics, gene mapping, identification of mutations
XX responsible for genetic disorders or other traits and to assess
XX biodiversity.
XX Claim 1; SEQ ID NO 5355; 103pp; English.
XX The invention relates to isolated polynucleotide (I) and polypeptide (II)
XX sequences. (I) is useful as hybridisation probes, polymerase chain
XX reaction (PCR) primers, oligomers, and for chromosome and gene mapping,
XX and in recombinant production of (II). The polynucleotides are also used
XX in diagnostics as expressed sequence tags for identifying expressed
XX genes. (I) is useful in gene therapy techniques to restore normal
XX activity of (II) or to treat disease states involving (II). (II) is
XX useful for generating antibodies against it, detecting or quantitating a
XX polypeptide in tissue, as molecular weight markers and as a food
XX supplement. (II) and its binding partners are useful for treating disorders
XX of sites expressing (II). (I) and (II) are useful for biological actions. The
XX involving aberrant protein expression or biological actions in
XX polypeptide and polynucleotide sequences have applications in
XX diagnostics, forensics, gene mapping, identification of mutations
XX and to produce other types of data and products dependent on DNA and
XX amino acid sequences. AAS64197-AAS94564 represent novel human diagnostic
XX coding sequences of the invention. Note: The sequence data for this
XX patent did not appear in the printed specification, but was obtained in
XX electronic format directly from WIPO at
XX ftp.wipo.int/pub/published_pct_sequences
XX
XX Sequence 873 BP; 235 A; 191 C; 229 G; 218 T; 0 U; 0 Other;
Query Match 19.7%; Score 31.4; DB 5; Length 873;
Best Local Similarity 53.7%; Pred. No. 19;
Matches 65; Conservative 0; Mismatches 56; Indels 0; Gaps 0;
QY 37 AGAAGAGCCTCAACCATTTGAAATGCCCTCAACAGCAGCTCAAAAGCTACAGAAATCTATTT 96
DB 207 AAAGAAACATATACCATTAATAAATTTGCATATAGGTATTAATATCTTCCCAATCATC 148
QY 97 ATCAATTTCTGTCTCATCTTTAATATGCTCTTGTGATCTGTATCATCGATGCTTCTC 156
DB 147 TTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTC 88
QY 157 T 157

RESULT 36
ADW94142
ID ADW94142 standard; DNA; 6025 BP.
XX
AC ADW94142;
XX
DT 21-APR-2005 (first entry)
XX
DE Staphylococcus aureus proliferation-required operon, SEQ ID 76.
XX
KW Operon; cell proliferation; microorganism; ds.
XX
OS Staphylococcus aureus.
XX
PN US2005026189-A1.
XX
PD 03-FEB-2005.
XX
PF 28-MAY-2004; 2004US-00857625.
XX
PR 29-MAY-2003; 2003US-0474768P.
XX
PA (WANG/) WANG L.
PA (ZAMU/) ZAMUDIO C.
XX
PI Wang L, Zamudio C;
XX
XX WPI; 2005-151156/16.
XX
XX Predicting operons of prokaryotes, by segregating consecutive genes of
XX organism, into bins based on their orientation, performing composite
XX operon prediction analysis, associating genes between operon boundaries
XX as putative operons.
XX
XX Example 7; SEQ ID NO 76; 116pp; English.
XX
XX The present invention relates to a method (M1) for predicting operons of
XX target prokaryotes. The method comprises identifying consecutive genes of
XX an organism's genome, determining the orientation of a gene in the genome
XX relative to its flanking genes, segregating the genes into bins based on
XX their orientation, performing composite operon prediction analysis,
XX determining operon boundaries by identifying gene pairs with confidence
XX scores below specific threshold and associating genes between boundaries
XX as putative operons. Also claimed is a computer-based system (I) for
XX carrying out (M1). (M1) is useful for identifying a gene that is required
XX for proliferation of a microorganism and in cell-based assays. ADW94067-
XX ADW94260 are proliferation-required operons from Staphylococcus aureus,
XX predicted using the method of the invention. ADW94261-ADW94610 are
XX proliferation-required genes, and ADW94611-ADW94884 are the encoded
XX proteins, from the predicted operons of the invention. Note: The sequence
XX data for this patent did not form part of the printed specification, but
XX was obtained in electronic format directly from USPTO at
XX seqdata.uspto.gov/sequence.html?DocID=20050026189.
XX
XX Sequence 6025 BP; 2262 A; 783 C; 1086 G; 1894 T; 0 U; 0 Other;
Query Match 20.0%; Score 31.8; DB 14; Length 6025;
Best Local Similarity 61.4%; Pred. No. 26;
Matches 51; Conservative 0; Mismatches 32; Indels 0; Gaps 0;
QY 36 AAGAAGCCTCAACCATTTGAAATGCCCTCAACAGCAGCTCAAAAGCTACAGATCTATT 95
DB 2301 ACGAAGAACTGAAATTTTGAATGGGTGGATATCATGTCAAATATATGTCAGATGTA 2360
QY 96 TATCAATTTCTGTCTCATCTTAA 118
DB 2361 CTTCAATTACTCTATAAAATAA 2383
RESULT 37
AAS69551/C
ID AAS69551 standard; cDNA; 873 BP.

Db 87 T 87

RESULT 38
AAS69244/c
ID AAS69244 standard; cDNA; 873 BP.
XX
XX AAS69244;
AC
XX
XX
XX 13-FEB-2002 (first entry)
DT
XX
XX DNA encoding novel human diagnostic protein #5048.
DE
XX
XX Human; chromosome mapping; gene mapping; gene therapy; forensic;
KW food supplement; medical imaging; diagnostic; genetic disorder; ss.
XX
XX Homo sapiens.
XX
XX WO200175067-A2.
XX
XX 11-OCT-2001.
XX
XX 30-MAR-2001; 2001WO-US008631.
XX
XX 31-MAR-2000; 2000US-00540217.
XX
XX 23-AUG-2000; 2000US-00649167.
XX
XX (HYSE-) HYSEQ INC.
XX
XX Dmanac RT, Liu C, Tang YT;
XX
XX WPI; 2001-639362/73.
XX
XX P-PSDB; ABG05057.
XX
XX New isolated polynucleotide and encoded polypeptides, useful in
PT diagnostics, forensics, gene mapping, identification of mutations
PT responsible for genetic disorders or other traits and to assess
PT biodiversity.
XX
XX Claim 1; SEQ ID NO 5048; 103pp; English.
XX
XX The invention relates to isolated polynucleotide (I) and polypeptide (II)
CC sequences. (I) is useful as hybridisation probes, polymerase chain
CC reaction (PCR) primers, oligomers, and for chromosome and gene mapping,
CC and in recombinant production of (II). The polynucleotides are also used
CC in diagnostics as expressed sequence tags for identifying expressed
CC genes. (I) is useful in gene therapy techniques to restore normal
CC activity of (II) or to treat disease states involving (II). (II) is
CC useful for generating antibodies against it, detecting or quantitating a
CC polypeptide in tissue, as molecular weight markers and as a food
CC supplement. (II) and its binding partners are useful in medical imaging
CC of sites expressing (II). (I) and (II) are useful for treating disorders
CC involving aberrant protein expression or biological activity. The
CC polypeptide and polynucleotide sequences have applications in
CC diagnostics, forensics, gene mapping, identification of mutations
CC responsible for genetic disorders or other traits to assess biodiversity
CC and to produce other types of data and products dependent on DNA and
CC amino acid sequences. AAS64197-AAS94564 represent novel human diagnostic
CC coding sequences of the invention. Note: The sequence data for this
CC patent did not appear in the printed specification, but was obtained in
CC electronic format directly from WIPO at
CC ftp.wipo.int/pub/published_pct_sequences
XX
XX Sequence 873 BP; 235 A; 191 C; 229 G; 218 T; 0 U; 0 Other;
Query Match 19.7%; Score 31.4; DB 5; Length 873;
Best Local Similarity 53.7%; Pred. No. 19;
Matches 65; Conservative 0; Mismatches 56; Indels 0; Gaps 0;

QY 37 AGAAGAGCTCAACCATTAATGCTCTCAACAGCAGCTCAACATCAATCTATT 96
DB 207 AAAGAACATACCAATTAATAAATGATATAGGTATTAATAATCTTCCCAATCATC 148

QY 97 ATCAATTCTGCTCATCTTAATATGCTCTTCTGATCTGATCATCATGATGCTTCTC 156
DB 147 TTCTTC 88

QY 157 T 157
DB 87 T 87

RESULT 39
AAS75469/c
ID AAS75469 standard; cDNA; 873 BP.
XX
XX AAS75469;
AC
XX
XX 13-FEB-2002 (first entry)
DT
XX
XX DNA encoding novel human diagnostic protein #11273.
DE
XX
XX Human; chromosome mapping; gene mapping; gene therapy; forensic;
KW food supplement; medical imaging; diagnostic; genetic disorder; ss.
XX
XX Homo sapiens.
XX
XX WO200175067-A2.
XX
XX 11-OCT-2001.
XX
XX 30-MAR-2001; 2001WO-US008631.
XX
XX 31-MAR-2000; 2000US-00540217.
XX
XX 23-AUG-2000; 2000US-00649167.
XX
XX (HYSE-) HYSEQ INC.
XX
XX Dmanac RT, Liu C, Tang YT;
XX
XX WPI; 2001-639362/73.
XX
XX P-PSDB; ABG11282.
XX
XX New isolated polynucleotide and encoded polypeptides, useful in
PT diagnostics, forensics, gene mapping, identification of mutations
PT responsible for genetic disorders or other traits and to assess
PT biodiversity.
XX
XX Claim 1; SEQ ID NO 11273; 103pp; English.
XX
XX The invention relates to isolated polynucleotide (I) and polypeptide (II)
CC sequences. (I) is useful as hybridisation probes, polymerase chain
CC reaction (PCR) primers, oligomers, and for chromosome and gene mapping,
CC and in recombinant production of (II). The polynucleotides are also used
CC in diagnostics as expressed sequence tags for identifying expressed
CC genes. (I) is useful in gene therapy techniques to restore normal
CC activity of (II) or to treat disease states involving (II). (II) is
CC useful for generating antibodies against it, detecting or quantitating a
CC polypeptide in tissue, as molecular weight markers and as a food
CC supplement. (II) and its binding partners are useful in medical imaging
CC of sites expressing (II). (I) and (II) are useful for treating disorders
CC involving aberrant protein expression or biological activity. The
CC polypeptide and polynucleotide sequences have applications in
CC diagnostics, forensics, gene mapping, identification of mutations
CC responsible for genetic disorders or other traits to assess biodiversity
CC and to produce other types of data and products dependent on DNA and
CC amino acid sequences. AAS64197-AAS94564 represent novel human diagnostic
CC coding sequences of the invention. Note: The sequence data for this
CC patent did not appear in the printed specification, but was obtained in
CC electronic format directly from WIPO at
CC ftp.wipo.int/pub/published_pct_sequences
XX
XX Sequence 873 BP; 235 A; 191 C; 229 G; 218 T; 0 U; 0 Other;
Query Match 19.7%; Score 31.4; DB 5; Length 873;
Best Local Similarity 53.7%; Pred. No. 19;
Matches 65; Conservative 0; Mismatches 56; Indels 0; Gaps 0;

Db 2510 TTGAGTTATATTAAGAATTTCTTAAATATATATTTAAGATATCTTTCTGTCAGAGTA 2569
142 A 142
2570 A 2570

RESULT 42
ABL32288/c
ID ABL32288 standard; DNA; 5875 BP.
AC ABL32288;
XX
DT 26-MAR-2002 (first entry)
XX
DE Human immune system associated gene SEQ ID NO: 261.
XX
KW Human; immune system disease; cytosine methylation; antiasthmatic;
KW antiarteriosclerotic; antianemic; cytostatic; nootropic;
KW neuroprotective; anti-HIV; anticonvulsant; ophthalmological;
KW antirheumatic; antiarthritic; antidiabetic; antipeptidic;
KW antiinflammatory; cancer; eye disease; arteriosclerosis; anaemia;
KW acute myeloid leukaemia; Alzheimer's disease; AIDS; epilepsy;
KW neurofibromatosis; rheumatoid arthritis; psoriasis; bowel disease; gene;
KW db.
XX
OS Homo sapiens.
XX
PN WO200200928-A2.
XX
PD 03-JAN-2002.
XX
PF 02-JUL-2001; 2001WO-EP007537.
XX
PR 30-JUN-2000; 2000DE-01032529.
XX
PR 01-SEP-2000; 2000DE-01043826.
XX
PA (EPIG-) EPIGENOMICS AG.
XX
PI Olek A, Piepenbrock C, Berlin K;
XX
XX WPI; 2002-130909/17.
XX
PT Nucleic acid comprising fragment of chemically modified gene, useful for
PT diagnosis and treatment of diseases associated with abnormal cytosine
PT methylation.
XX
PS Claim 1; SEQ ID NO 261; 32pp + Sequence Listing; German.
XX
CC The present invention provides a number of human immune system associated
CC genes which are modified by the methylation of cytosines. The sequences
CC can be used in the diagnosis and treatment of immune system disorders,
CC including eye diseases such as retinopathy, neovascular glaucoma and
CC macular degeneration, arteriosclerosis, anaemia, cancer, acute myeloid
CC leukaemia, Alzheimer's disease, AIDS, epilepsy, neurofibromatosis,
CC rheumatoid arthritis, psoriasis and inflammatory/ulcerative bowel
CC diseases. The present sequence is a gene of the invention
XX
SQ Sequence 5875 BP; 1930 A; 27 C; 1031 G; 2887 T; 0 U; 0 Other;
Query Match 19.7%; Score 31.4; DB 6; Length 5875;
Best Local Similarity 56.2%; Pred. No. 34;
Matches 59; Conservative 0; Mismatches 46; Indels 0; Gaps 0;

QY 21 CACTCGCTCAGCTATAAGAAGCGCTCAACCAATTTGAATGCTCAACAGCAGTCAGAAA 80
421 CATACTTTCTCTTTAAATAAATACTAATTAATTAATTCACCTCAACACCACTTCAAAA 362

QY 81 GCTACAGATCTATTATCAATTTCTGCTCATCTTAATATGCT 125

Db 361 ACTACTCACTATTCTTCTAAATTAATTTCCCCCATAAATTTCT 317

RESULT 43
ACN44322/c
ID ACN44322 standard; DNA; 84073 BP.
XX
AC ACN44322;
XX
DT 18-NOV-2004 (first entry)
XX
DE Human genomic sequence HCG28354.
XX
KW Cytostatic; carcinoma; lymphoma; cancer; human; gene; ss.
XX
OS Homo sapiens.
XX
PN WO2003073826-A2.
XX
PD 12-SEP-2003.
XX
PR 28-FEB-2003; 2003WO-US006235.
XX
PR 01-MAR-2002; 2002US-00087192.
XX
PA (SAGR-) SAGRES DISCOVERY.
XX
PI Morris DW;
XX
XX WPI; 2003-328604/31.
XX
DR Recombinant nucleic acid useful for diagnosis and treatment of carcinoma
XX comprises a nucleotide sequence.
XX
PS Claim 1; SEQ ID NO 712; Opp; English.
XX
CC The present invention relates to novel DNA and protein sequences which
CC are associated with carcinomas. The sequences are useful for: (i) for
CC screening drug candidates, (ii) for screening of bioactive agent capable
CC of binding to Carcinoma Associated Protein (CAP); (iii) for screening of
CC a bioactive agent capable of modulating the activity of CAP; (iv) for
CC evaluating the effect of a candidate carcinoma drug; (v) for diagnosing
CC carcinoma; (vi) for inhibiting the activity of CAP; (vii) for treating
CC carcinoma; (viii) for neutralizing the effect of CAP; (ix) as a biochip;
CC (x) for diagnosing carcinoma or a propensity to carcinoma; and (xi) for
CC determining Carcinoma Associated (CA) gene copy number. In addition, the
CC CA genes are useful as DNA vaccines and the CAP are useful as markers of
CC carcinoma including lymphoma. The present sequence is one such CA coding
CC sequence. Note: This patent is an equivalent to basic patent
CC US2002182586A1, for which no sequence data was published
XX
SQ Sequence 84073 BP; 25133 A; 15743 C; 16036 G; 27161 T; 0 U; 0 Other;
Query Match 19.6%; Score 31.2; DB 11; Length 84073;
Best Local Similarity 58.7%; Pred. No. 89;
Matches 54; Conservative 0; Mismatches 38; Indels 0; Gaps 0;

QY 37 AGAAGAGCGCTCAACCAATTTGAATGCTCAACAGCAGTCAGAAAAGCTACAGATCTATTT 96
Db 28668 AGTAGAGATACAGCCACACAAAGAAATCCAGGTCATATAAACCAACAGAGTTATCT 28609

QY 97 ATCAATTTCTGCTCATCTTAATATGCTCTT 128

Db 28608 AACAACTTTGAATCTTGTATCTGAGTCTT 28577

RESULT 44
ADR60594/c
ID ADR60594 standard; cDNA; 1269 BP.
XX
AC ADR60594;
XX
DT 02-DEC-2004 (first entry)
XX
DE Cotton cDNA sequence, SEQ ID 1475.

XX Cotton; ss; plant; cold tolerance; growth rate; cell cycle pathway;
KW drought tolerance; plant disease resistance; galactomannan; lignin;
KW plant growth regulator; heat tolerance; herbicide tolerance;
KW homologous recombination; extreme osmotic condition tolerance;
KW pathogen resistance; pest resistance; yield; photosynthesis; seed oil;
KW stress resistance.
XX Gossypium hirsutum.
OS US2004181830-A1.
XX 16-SEP-2004.
XX 29-JAN-2004; 2004US-00767795.
XX 07-MAY-2001; 2001US-00849529.
XX 12-DEC-2001; 2001US-00021323.
XX (KOVA//) KOVALIC D K.
PA (ZHOU//) ZHOU Y.
PA (CAO//) CAO Y.
XX Kovalic DK, Zhou Y, Cao Y;
PI WPI; 2004-667718/65.
XX New recombinant nucleic acid molecules and polypeptides from Gossypium
PT hirsutum, useful for producing plants with improved biological
PT characteristics (e.g. improved plant cold or drought tolerance).
XX Claim 1; SEQ ID NO 1475; 14pp; English.
XX The invention relates to a recombinant polynucleotide comprising any of
CC the 58798 Cotton plant cDNA sequences mentioned in the specification.
CC Also a recombinant polypeptide comprising any of the 58798 amino acid
CC sequences mentioned in the specification and producing a plant having an
CC improved property. Producing a plant having an improved property
CC comprises transforming a plant with a recombinant construct comprising a
CC promoter region functional in a plant cell operably joined to a
CC polynucleotide comprising a coding sequence for a polypeptide associated
CC with the property, and growing the transformed plant. The polypeptide is
CC useful for improving plant cold tolerance, manipulating growth rate in
CC plant cells by modification of the cell cycle pathway, improving plant
CC drought tolerance, providing increased resistance to plant disease,
CC producing galactomannan (or lignin or plant growth regulators), improving
CC plant heat tolerance, improving plant tolerance to herbicides, increasing
CC the rate of homologous recombination in plants, improving plant tolerance
CC to extreme osmotic conditions or to pathogens or pests, improving yield
CC by modification of photosynthesis, modifying seed oil or protein yield
CC and/or content, improving yield by modification of carbohydrate, nitrogen
CC or phosphorus use and/or uptake, or improving yield by providing improved
CC plant growth and development under at least one stress condition. The
CC polynucleotide and polypeptide may also be used in recombinant DNA
CC constructs, in physical arrays of molecules, as plant breeding markers,
CC or in computer-based storage and analysis systems. The present sequence
CC is a Cotton plant cDNA of the invention. NOTE: The sequence data for this
CC patent did not form part of the printed specification, but was obtained
CC in electronic format directly from USPTO at
CC seqdata.uspto.gov/sequences.html?docID=20040181830. However only 6585
CC polynucleotide sequences were available, the remaining 52213
CC polynucleotides and all 58798 protein sequences were not present.
XX Sequence 1269 BP; 345 A; 232 C; 284 G; 408 T; 0 U; 0 Other;
SQ
Query Match 19.5%; Score 31; DB 13; Length 1269;
Best Local Similarity 68.3%; Pred. No. 28;
Matches 43; Conservative 0; Mismatches 20; Indels 0; Gaps 0;
QY 93 ATTATCAATTCCTGCTCATCTTAATGATCTCTTGTGATCTGATCATCGTGCT 152
DB 279 ATCCATGAATTCCTCTTCTCACTTATCTTCTTCTGATTTGATCACCTCTTCCT 220

QY 153 TCT 155
DB 219 CCT 217
RESULT 45
ABL34015/C
ID ABL34015 standard; DNA; 6182 BP.
XX
AC ABL34015;
XX 26-MAR-2002 (first entry)
XX Human immune system associated gene SEQ ID NO: 1988.
XX Human; immune system disease; cytosine methylation; antiasthmatic;
KW antiarteriosclerotic; antianaemic; cytostatic; nootropic;
KW neuroprotective; anti-HIV; anticonvulsant; ophthalmological;
KW antirheumatic; antiarthritis; antidiabetic; antipsoriatic;
KW antiinflammatory; cancer; eye disease; arteriosclerosis; anaemia;
KW acute myeloid leukaemia; Alzheimer's disease; AIDS; epilepsy;
KW neurofibromatosis; rheumatoid arthritis; psoriasis; bowel disease; gene;
KW ds.
XX Homo sapiens.
OS WO200200928-A2.
XX 03-JAN-2002.
PD 02-JUL-2001; 2001WO-EP007537.
XX 30-JUN-2000; 2000DE-01032529.
PR 01-SEP-2000; 2000DE-01043826.
XX (EPIG-) EPIGENOMICS AG.
PI Olek A, Piepenbrock C, Berlin K;
XX WPI; 2002-130909/17.
XX Nucleic acid comprising fragment of chemically modified gene, useful for
PT diagnosis and treatment of diseases associated with abnormal cytosine
PT methylation.
XX Claim 1; SEQ ID NO 1988; 32pp + Sequence Listing; German.
XX The present invention provides a number of human immune system associated
CC genes which are modified by the methylation of cytosines. The sequences
CC can be used in the diagnosis and treatment of immune system disorders,
CC including eye diseases such as retinopathy, neovascular glaucoma and
CC macular degeneration, arteriosclerosis, anaemia, cancer, acute myeloid
CC leukaemia, Alzheimer's disease, AIDS, epilepsy, neurofibromatosis,
CC rheumatoid arthritis, psoriasis and inflammatory/ulcerative bowel
CC diseases. The present sequence is a gene of the invention
XX
SQ Sequence 6182 BP; 1934 A; 37 C; 1059 G; 3152 T; 0 U; 0 Other;
Query Match 19.5%; Score 31; DB 6; Length 6182;
Best Local Similarity 52.8%; Pred. No. 46;
Matches 67; Conservative 0; Mismatches 60; Indels 0; Gaps 0;
QY 1 ATGAGAGAAAGTCCAATACCTCACTCGCTCAGCTATAGAGAGCGCTCAACCATTTGAATG 60
DB 3341 ATATATAAATTTCAATATCTATAAATTTTAAACCAAAAAACCATATCAAAACAATA 3282
QY 61 CCTCAACAGCAGCTCAAAAGCTACAGAATCTATTTTATCAATTTCTGCTCATCTTAATA 120
DB 3281 AAACACAAATAACATCAACTTCCAAAAAATAATTTATATCTTTTAAATATACAAAAA 3222
QY 121 TGTCTCT 127
DB 3221 TATCCCT 3215

XX	nuclear fertility; plant; male-fertility; male-fertility restorer; marker; transformation; radish; Rfo; petunia; Rf; Brassica napus; ds; gene.
OS	Raphanus sativum.
XX	WO2004006655-A2.
XX	22-JAN-2004.
XX	16-JAN-2003; 2003WO-US001343.
XX	12-JUL-2002; 2002US-00195144.
PR	15-JAN-2003; 2003US-00345072.
XX	(UYMC-) UNIV MCGILL.
PA	(DNAL-) DNA LANDMARKS INC.
PA	(BADI) BASF PLANT SCI GMBH.
XX	Brown GG, Formanova N, Deny C, Landry BS, Cheung W, Jin H; Lai FM, Leforest M;
PI	WPI; 2004-122713/12.
XX	Using a plant male-fertility restorer as a marker for transformation by providing an expression cassette encoding a plant male fertility restorer and transforming cytoplasmic male sterile plant cells with the expression cassette.
XX	Claim 15; SEQ ID NO 87; 309pp; English.
XX	The invention relates to a novel method for using a plant male-fertility restorer as a marker for transformation. Using a plant male-fertility restorer as a marker for transformation comprises: providing an expression cassette for a male fertility restorer; transforming cytoplasmic male sterile plants with the expression cassette; and identifying plants from step (2) that form seeds when self-pollinated. The male fertility restorer is a radish Rfo or a petunia Rf. The plant is Brassica napus. The expression cassette is covalently linked to a sequence of interest. The expression cassette is co-transformed into the plant cells with a nucleotide sequence of interest. The method is useful for using a plant male-fertility restorer as a marker for transformation. The present sequence is used in the exemplification of the invention.
XX	Sequence 271990 BP; 89601 A; 47321 C; 46931 G; 88077 T; 0 U; 60 Other;
SQ	Query Match 19.5%; Score 31; DB 12; Length 271990;
SS	Best Local Similarity 53.8%; Pred. No. 1.5e+02;
SS	Matches 64; Conservative 0; Mismatches 55; Indels 0; Gaps 0;
QY	7 AAGTCCAACTACTCTACTCGCTCAGCTATAGAAGAGCGCTCAACCAATTGAAATGCCTCAA 66
Db	94279 AAGTCAAGAGCATATAATCTCGTTTCAAAATCCAAGCTTCAATAATACAATCCTGAGA 94222
QY	67 CAAGCAGCTCAAAAGCTACAGAACTCTATTATCAATTTCTGCTCATCTTAATATGTC 125
Db	94219 AAGTACCTCCACTTTCTAGCTTACATTGCTCAATTTTCTTCTCTCTAAATCAGTTT 94161
RESULT 48	
ID	ADNR61212/c
XX	ID ADNR61212 standard; cDNA; 437 BP.
XX	ADNR61212;
XX	02-DEC-2004 (first entry)
XX	Cotton cDNA sequence, SEQ ID 1993.
DE	Cotton; ss; plant; cold tolerance; growth rate; cell cycle pathway; drought tolerance; plant disease resistance; galactomannan; lignin; plant growth regulator; heat tolerance. herbicide tolerance.

```

RESULT 46
ADD25213/c
ID .ADD25213 standard; DNA; 271990 BP.
XX AC ADD25213;
XX DT 15-JAN-2004 (first entry)
XX DE Fertility restorer protein genomic DNA sequence.
XX KW fertility restorer protein; male sterile plant; viable pollen production;
XX KW selection marker; ds; gene.
XX OS Unidentified.
XX PN WO2003006622-A2.
XX PD 23-JAN-2003.
XX PF 12-JUL-2002; 2002WO-US022217.
XX PR 12-JUL-2001; 2001US-0305026P.
XX PR 13-JUL-2001; 2001US-0305363P.
XX PR 30-JUL-2001; 2001US-0308736P.
XX (UYMC-) UNIV MCGILL.
XX PA (DNAL-) DNA LANDMARKS INC.
XX PI Brown GG, Formanova N, Dendy C, Landry BS, Cheung W, Jin H;
XX MPI; 2003-221734/21.
XX New nuclear fertility restorer genes, useful for restoring fertility in
XX cytoplasmic male-sterile plants such as Brassica napus plants, or for
XX increasing production of viable pollen in a plant.
XX Claim 1; SEQ ID NO 87; 191pp; English.
XX The invention comprises the amino acid and coding sequences of isolated
XX fertility restorer proteins. The DNA and protein sequences of the
XX invention are useful for restoring fertility in male sterile plants, such
XX as Brassica napus plants. The DNA and protein sequences of the invention
XX are useful for increasing production of viable pollen in a plant. The DNA
XX and protein sequences are also useful as selection markers to identify
XX transformed plant cells. The present genomic DNA sequence contains coding
XX sequences for fertility restorer proteins of the invention.
XX SQ Sequence 271990 BP; 89597 A; 47325 C; 46930 G; 88078 T; 0 U; 60 Other;
Query Match 19.5%; Score 31; DB 10; Length 271990;
Best Local Similarity 53.8%; Pred. No. 1.5e+02;
Matches 64; Conservative 0; Mismatches 55; Indels 0; Gaps 0;
QY 7 AAAGTCCAAATACCTCACTCGCTCAGCTATAAGAGAGCTCAACCATTTGAATGCTCAA 66
DB 94279 AAAGTCAAGAAGCATATCTCGTTTCAAAATCCAGCTTCAATATACAAATCTCTGAGA 94220
QY 67 CAAGCACGTCAAAGCTACAGAAATCTATTTATPAAATTTCTGTCTCATCTTAATATGCT 125
DB 94219 AAAGTACCTCCACTTTCTAGCTTACATTTGCTCAATTTCTTCTTCTAATCAGTTT 94161
RESULT 47
ADN61228/c
ID ADN61228 standard; DNA; 271990 BP.
XX AC ADN61228;
XX DT 01-JUL-2004 (first entry)
XX DE Radish nuclear fertility restorer Rfo Rfo locus SEQ ID NO:87.

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Search completed: December 8, 2005, 00:35:17
Job time : 487 secs

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OM nucleic - nucleic search, using sw model

Run on: December 8, 2005, 00:19:41 ; Search time 140 Seconds
(without alignments)

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Searched: 1303057 seqs, 888780828 residues

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Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 100 summaries

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9: /cgm2_6/ptodata/1/ina/backfiles1.seq.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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1	159	100.0	480	3	US-09-513-999C-10799 Sequence 10799, A
2	159	100.0	1635	3	US-09-949-016-1439 Sequence 1439, Ap
3	159	100.0	16062	3	US-09-949-016-13181 Sequence 13181, A
4	144.6	90.9	159	3	US-09-949-872B-13 Sequence 13, Appl
5	143	89.9	159	3	US-09-949-872B-9 Sequence 9, Appl
6	83	52.2	315	3	US-09-124-671-26 Sequence 26, Appl
7	34.6	21.8	2071	3	US-09-023-023-1 Sequence 1, Appl
8	33.2	20.9	601	3	US-09-949-016-135505 Sequence 135505, A
9	33.2	20.9	601	3	US-09-949-016-135525 Sequence 135525, A
10	33.2	20.9	75929	3	US-09-949-016-15543 Sequence 15543, A
11	33.2	20.9	75929	3	US-09-949-016-15543 Sequence 15543, A
12	32.2	20.3	3713	2	US-08-100-709-1 Sequence 1, Appl
13	32.2	20.3	3713	2	US-08-176-865-1 Sequence 1, Appl
14	32.2	20.3	3713	2	US-08-474-038-1 Sequence 1, Appl
15	32.2	20.3	3713	2	US-08-779-046-1 Sequence 1, Appl
16	32.2	20.3	3713	2	US-08-881-340-1 Sequence 1, Appl
17	32.2	20.3	59240	3	US-09-949-016-11933 Sequence 11933, A
18	31.8	20.0	1421	3	US-08-956-171E-283 Sequence 283, App
19	31.8	20.0	1421	3	US-08-781-986A-283 Sequence 283, App
20	31.6	19.9	264358	3	US-09-949-016-15725 Sequence 15725, A
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22	31.4	19.7	601	3	US-09-949-016-15725 Sequence 15725, A
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24	31.4	19.7	601	3	US-09-949-016-15725 Sequence 15725, A

25	30.8	19.4	2090	2	US-08-439-814-1 Sequence 1, Appl
26	30.4	19.1	55061	3	US-09-949-016-14704 Sequence 14704, A
27	30.4	19.1	55061	3	US-09-949-016-14705 Sequence 14705, A
28	30.4	19.1	55061	3	US-09-949-016-14706 Sequence 14706, A
29	30.4	19.1	55061	3	US-09-949-016-14707 Sequence 14707, A
30	30.4	19.1	55061	3	US-09-949-016-14708 Sequence 14708, A
31	30.4	19.1	55061	3	US-09-949-016-14709 Sequence 14709, A
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36	30.4	19.1	278866	3	US-09-949-016-13926 Sequence 13926, A
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40	30.4	19.1	278866	3	US-09-949-016-14702 Sequence 14702, A
41	30.4	19.1	278866	3	US-09-949-016-14703 Sequence 14703, A
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46	30.2	19.0	161914	3	US-09-949-016-12685 Sequence 12685, A
47	30	18.9	601	3	US-08-998-416-295 Sequence 196215, A
48	30	18.9	859	3	US-09-949-016-12542 Sequence 12542, A
49	30	18.9	173787	3	US-09-949-016-17302 Sequence 17302, A
50	30	18.9	173791	3	US-09-949-016-12201 Sequence 12201, A
51	30	18.9	227390	3	US-09-949-016-13365 Sequence 13365, A
52	30	18.9	227391	3	US-09-621-976-9957 Sequence 9957, Ap
53	29.8	18.7	380	3	US-09-949-016-2218 Sequence 2218, Ap
54	29.8	18.7	972	3	US-09-949-016-116 Sequence 116, App
55	29.6	18.6	601	3	US-09-949-016-134542 Sequence 134542, A
56	29.6	18.6	601	3	US-09-949-016-12779 Sequence 12779, A
57	29.6	18.6	1539	3	US-09-949-016-15511 Sequence 15511, A
58	29.6	18.6	17864	3	US-09-949-016-74856 Sequence 74856, A
59	29.6	18.5	601	3	US-09-949-016-75055 Sequence 75055, A
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61	29.4	18.5	601	3	US-09-949-016-75453 Sequence 75453, A
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64	29.4	18.5	601	3	US-09-949-016-106409 Sequence 106409, A
65	29.4	18.5	601	3	US-09-949-016-106608 Sequence 106608, A
66	29.4	18.5	601	3	US-09-949-016-107006 Sequence 107006, A
67	29.4	18.5	601	3	US-09-949-016-107048 Sequence 107048, A
68	29.4	18.5	601	3	US-09-949-016-107132 Sequence 107132, A
69	29.4	18.5	601	3	US-09-949-016-107174 Sequence 107174, A
70	29.4	18.5	601	3	US-09-949-016-107216 Sequence 107216, A
71	29.4	18.5	601	3	US-09-949-016-107258 Sequence 107258, A
72	29.4	18.5	601	3	US-10-104-047-1798 Sequence 1798, Ap
73	29.4	18.5	601	3	US-08-956-171B-416 Sequence 416, App
74	29.4	18.5	601	3	US-08-781-986A-416 Sequence 416, App
75	29.4	18.5	601	3	US-09-621-976-2784 Sequence 2784, Ap
76	29.4	18.5	601	3	US-09-949-016-17099 Sequence 17099, A
77	29.4	18.5	601	3	US-09-949-016-12497 Sequence 12497, A
78	29.4	18.5	601	3	US-09-248-796A-610 Sequence 610, App
79	29.2	18.4	555	3	US-09-949-016-15258 Sequence 15258, A
80	29.2	18.4	76563	3	US-09-949-016-13418 Sequence 13418, A
81	29.2	18.4	78269	3	US-09-949-016-15980 Sequence 15980, A
82	29	18.2	456	3	US-09-949-016-13632 Sequence 13632, A
83	29	18.2	48149	3	US-09-949-016-193542 Sequence 193542, A
84	29	18.2	236474	3	US-08-851-567B-27 Patent No. 5198347-5
85	29	18.2	239527	3	US-09-949-016-13256 Sequence 13256, A
86	29	18.2	300402	3	US-09-949-016-113080 Sequence 113080, A
87	28.8	18.1	601	3	US-09-949-016-13749 Sequence 13749, A
88	28.8	18.1	1881	3	US-09-949-016-1132 Sequence 1132, App
89	28.8	18.1	4084	9	US-08-851-567B-25 Sequence 25, Appl
90	28.8	18.1	5050	3	US-09-949-016-11874 Sequence 11874, A
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92	28.8	18.1	23222	3	US-09-949-016-13256 Sequence 13256, A
93	28.8	18.1	25922	3	US-09-949-016-113080 Sequence 113080, A
94	28.8	18.1	49416	3	US-09-949-016-113080 Sequence 113080, A
95	28.8	18.1	50368	3	US-09-949-016-113080 Sequence 113080, A
96	28.8	18.1	105733	3	US-09-949-016-113080 Sequence 113080, A
97	28.8	18.1	156324	3	US-09-949-016-113080 Sequence 113080, A

98 28.8 18.1 268449 3 US-09-949-016-17244 Sequence 17244, A
28.6 18.0 603 3 US-09-543-681A-2490 Sequence 2490, Ap
c 100 28.6 18.0 2533 3 US-10-104-047-130 Sequence 130, App

ALIGNMENTS

RESULT 1
US-09-513-999C-10799
; Sequence 10799, Application US/09513999C
; Patent No. 6783961
; GENERAL INFORMATION:
; APPLICANT: Dumas Milne Edwards, J.B.
; APPLICANT: Duclert, A.
; APPLICANT: Giordano, J.Y.
; TITLE OF INVENTION: Expressed Sequence Tags and Encoded Human Proteins.
; FILE REFERENCE: 59 US2.REG
; CURRENT APPLICATION NUMBER: US/09/513,999C
; CURRENT FILING DATE: 2000-02-24
; PRIOR APPLICATION NUMBER: US 60/122,487
; PRIOR FILING DATE: 1999-02-26
; NUMBER OF SEQ ID NOS: 36681
; SOFTWARE: Patent.pm
; SEQ ID NO 10799
; LENGTH: 480
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-513-999C-10799

Query Match 100.0%; Score 159; DB 3; Length 480;
Best Local Similarity 100.0%; Pred. No. 2.3e-40; Indels 0; Gaps 0;
Matches 159; Conservative 0; Mismatches 0

QY 1 ATGGAGAAAGTCCAAATACCTCAGCTCAGCTATAGAGAGCCCTCAACCAATTGAAATG 60
DB 196 ATGGAGAAAGTCCAAATACCTCAGCTCAGCTATAGAGAGCCCTCAACCAATTGAAATG 255

QY 61 CCTCAACAAGCAGCTCAAAAGCTACAGAATCTATTATCAATTTCTGCTCATCTTAATA 120
DB 256 CCTCAACAAGCAGCTCAAAAGCTACAGAATCTATTATCAATTTCTGCTCATCTTAATA 315

QY 121 TGTCTCTTGTGATCTGTATCATCGTGATGCTTCTCTGA 159
DB 316 TGTCTCTTGTGATCTGTATCATCGTGATGCTTCTCTGA 354

RESULT 2
US-09-949-016-1439
; Sequence 1439, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 1439
; LENGTH: 1635
; TYPE: DNA
; ORGANISM: Human
US-09-949-016-1439

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Best Local Similarity 100.0%; Pred. No. 3.4e-40; Indels 0; Gaps 0;
Matches 159; Conservative 0; Mismatches 0

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QY 61 CCTCAACAAGCAGCTCAAAAGCTACAGAATCTATTATCAATTTCTGCTCATCTTAATA 120
DB 242 CCTCAACAAGCAGCTCAAAAGCTACAGAATCTATTATCAATTTCTGCTCATCTTAATA 301

QY 121 TGTCTCTTGTGATCTGTATCATCGTGATGCTTCTCTGA 159
DB 302 TGTCTCTTGTGATCTGTATCATCGTGATGCTTCTCTGA 340

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US-09-949-016-13181
; Sequence 13181, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 13181
; LENGTH: 16062
; TYPE: DNA
; ORGANISM: Human
US-09-949-016-13181

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Best Local Similarity 100.0%; Pred. No. 7e-40; Indels 0; Gaps 0;
Matches 159; Conservative 0; Mismatches 0

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QY 121 TGTCTCTTGTGATCTGTATCATCGTGATGCTTCTCTGA 159
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RESULT 4
US-09-549-872B-13
; Sequence 13, Application US/09549872B
; Patent No. 6540996
; GENERAL INFORMATION:
; APPLICANT: Zwaal, Richard
; APPLICANT: Groenen, Jose
; APPLICANT: Bogaert, Thierry
; TITLE OF INVENTION: COMPOUND SCREENING METHODS
; FILE REFERENCE: D00590/70008 (JRV/RE)
; CURRENT APPLICATION NUMBER: US/09/549,872B
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: GB 9908670.4
; PRIOR FILING DATE: 1999-04-15

PRIOR APPLICATION NUMBER: US 60/129,596
PRIOR FILING DATE: 1999-04-15
PRIOR APPLICATION NUMBER: GB 9112736.7
PRIOR FILING DATE: 1999-06-01
NUMBER OF SEQ ID NOS: 39
SOFTWARE: Patent in Ver. 2.0
SEQ ID NO 13
LENGTH: 159
TYPE: DNA
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Description of Artificial Sequence: HUMANIZED PIG
OTHER INFORMATION: PUB cDNA
US-09-549-872B-13

Query Match 90.9%; Score 144.6; DB 3; Length 159;
Best Local Similarity 94.3%; Pred. No. 5.4e-36;
Matches 150; Conservative 0; Mismatches 9; Indels 0; Gaps 0;
QY 1 ATGGAGAAAGTCCAAATACCTCAGCTGCTAGCTATAGAGAGCTCAACCATTTGAAATG 60
DB 1 ATGGAGAAAGTCCAAATACCTCAGCTGCTAGCTATAGAGAGCTCAACCATTTGAAATG 60
QY 61 CCTCAACAGCAGCTCAAAAGCTACAGATCTATTATCAATTTCTGCTCATCTTAATA 120
DB 61 CCTCAACAGCAGCTCAAAAGCTACAGATCTATTATCAATTTCTGCTCATCTTAATA 120
QY 121 TGCTCTTGTGATCTGTATCATCGTATGCTTCTCTGA 159
DB 121 TGCTCTTGTGATCTGTATCATCGTATGCTTCTCTGA 159

RESULT 5
US-09-549-872B-9
Sequence 9, Application US/09549872B
Patent No. 6540996
GENERAL INFORMATION:
APPLICANT: Zwaal, Richard
APPLICANT: Groenen, Jose
APPLICANT: Bogardt, Thierry
TITLE OF INVENTION: COMPOUND SCREENING METHODS
FILE REFERENCE: D00590/70008 (JRV/RE)
CURRENT APPLICATION NUMBER: US/09/549,872B
CURRENT FILING DATE: 2000-04-14
PRIOR APPLICATION NUMBER: GB 9508670.4
PRIOR FILING DATE: 1999-04-15
PRIOR APPLICATION NUMBER: US 60/129,596
PRIOR FILING DATE: 1999-04-15
PRIOR APPLICATION NUMBER: GB 9912736.7
PRIOR FILING DATE: 1999-06-01
NUMBER OF SEQ ID NOS: 39
SOFTWARE: Patent in Ver. 2.0
SEQ ID NO 9
LENGTH: 159
TYPE: DNA
ORGANISM: Sus sp.
US-09-549-872B-9

Query Match 89.9%; Score 143; DB 3; Length 159;
Best Local Similarity 93.7%; Pred. No. 1.7e-35;
Matches 149; Conservative 0; Mismatches 10; Indels 0; Gaps 0;
QY 1 ATGGAGAAAGTCCAAATACCTCAGCTGCTAGCTATAGAGAGCTCAACCATTTGAAATG 60
DB 1 ATGGAGAAAGTCCAAATACCTCAGCTGCTAGCTATAGAGAGCTCAACCATTTGAAATG 60
QY 61 CCTCAACAGCAGCTCAAAAGCTACAGATCTATTATCAATTTCTGCTCATCTTAATA 120
DB 61 CCTCAACAGCAGCTCAAAAGCTACAGATCTATTATCAATTTCTGCTCATCTTAATA 120
QY 121 TGCTCTTGTGATCTGTATCATCGTATGCTTCTCTGA 159
DB 121 TGCTCTTGTGATCTGTATCATCGTATGCTTCTCTGA 159

RESULT 6

US-09-124-671-26
Sequence 26, Application US/09124671A
Patent No. 6160088
GENERAL INFORMATION:
APPLICANT: Rothman, James
APPLICANT: Mayhew, Mark
APPLICANT: Hoe, Mee
TITLE OF INVENTION: KDEL RECEPTOR INHIBITORS
FILE REFERENCE: 31488
CURRENT APPLICATION NUMBER: US/09/124,671A
CURRENT FILING DATE: 1998-07-29
NUMBER OF SEQ ID NOS: 42
SOFTWARE: FastSeq for Windows Version 3.0
SEQ ID NO 26
LENGTH: 315
TYPE: DNA
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: chimeric human PLB-KDEL
US-09-124-671-26

Query Match 52.2%; Score 83; DB 3; Length 315;
Best Local Similarity 100.0%; Pred. No. 1.5e-16;
Matches 83; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 74 GTCAAAAGCTACAGAAATCTATTATCAATTTCTGCTCATCTTAATATGCTTCTGA 133
DB 98 GTCAAAAGCTACAGAAATCTATTATCAATTTCTGCTCATCTTAATATGCTTCTGA 157
QY 134 TCTGTATCATCGTGATGCTTCTC 156
DB 158 TCTGTATCATCGTGATGCTTCTC 180

RESULT 7

US-09-023-023-1
Sequence 1, Application US/09023023
Patent No. 6121018
GENERAL INFORMATION:
APPLICANT: Kristine Kay Kikly
TITLE OF INVENTION: Interleukin-1 Beta Converting Enzyme Like Apoptosis Pr
NUMBER OF SEQUENCES: 2
CORRESPONDENCE ADDRESS:
ADDRESSEE: SmithKline Beecham Corporation
STREET: 709 Swedeland Road
CITY: King of Prussia
STATE: PA
COUNTRY: USA
ZIP: 19406
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FastSeq for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/023,023
FILING DATE: 12-FEB-1998
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 60/042,030
FILING DATE: March 27, 1997
ATTORNEY/AGENT INFORMATION:
NAME: Han, William T
REGISTRATION NUMBER: 34,344
REFERENCE/DOCKET NUMBER: GHS0013
TELECOMMUNICATION INFORMATION:
TELEPHONE: 610-270-5219
TELEFAX: 610-270-5090
TELEX:
INFORMATION FOR SEQ ID NO: 1:

```

; SEQUENCE CHARACTERISTICS:
; LENGTH: 2071 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
US-09-023-023-1
Query Match      21.8%; Score 34.6; DB 3; Length 2071;
Best Local Similarity 58.1%; Pred. No. 0.43; Indels 0; Gaps 0;
Matches 61; Conservative 0; Mismatches 44;

QY 34 ATAAGAAGAGCCTCAACCAATGAAATGCTCAACAGCAGCTCAAAAGCTACAGAACTCA 93
Db 1215 ATCAGAGAAATTCACCAATATATCAGCTTCAAGAGCATTTTATCAGCAGCATCCA 1274

QY 94 TTTATCAATTTCTGCTCATCTTAATATGCTCTCTTGTGCTGATCTGT 138
Db 1275 TGTTTAACTTTGCTTTTCATTTAAAGTGAAACATATGAACTGT 1319

RESULT 8
US-09-949-016-135505
; Sequence 135505, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; FILE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 135505
; LENGTH: 601
; TYPE: DNA
; ORGANISM: Human
US-09-949-016-135505
Query Match      20.9%; Score 33.2; DB 3; Length 601;
Best Local Similarity 54.0%; Pred. No. 0.8;
Matches 68; Conservative 0; Mismatches 58; Indels 0; Gaps 0;

QY 27 CTCAGCTATAAGAGAGCCTCAACCAATGAAATGCTCAACAGCAGCTCAAAAGCTACA 86
Db 115 CTCAGCCTTCCAAAGTGCCGGGATCACAGGCGTGAACACCAACCGCCGACCAAGTTCT 174

QY 87 GAATCTATTATCAATTTCTGCTCATCTTAATATGCTCTTGTGCTGATCTGTATCATCGT 146
Db 175 TTTTATATATTTCAGCTCTTCTCATTAATAAACTTTTAAGTTAATGAGCAGTGCTATTGT 234

QY 147 GATGCT 152
Db 235 AGTGCT 240

RESULT 9
US-09-949-016-135525
; Sequence 135525, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; FILE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 135525
; LENGTH: 601
; TYPE: DNA
; ORGANISM: Human
US-09-949-016-135525
Query Match      20.9%; Score 33.2; DB 3; Length 75929;
Best Local Similarity 54.0%; Pred. No. 3.7;
Matches 68; Conservative 0; Mismatches 58; Indels 0; Gaps 0;

QY 27 CTCAGCTATAAGAGAGCCTCAACCAATGAAATGCTCAACAGCAGCTCAAAAGCTACA 86
Db 31048 CTCAGCCTTCCAAAGTGCCGGGATCACAGGCGTGAACCAACCAACCGCCGACCAAGTTCT 31107

QY 87 GAATCTATTATCAATTTCTGCTCATCTTAATATGCTCTTGTGCTGATCTGTATCATCGT 146
Db 31108 TTTTATATATTTCAGCTCTTCTCATTAATAAACTTTAAAGTTAATGAGCAGTGCTATTGT 31167

QY 147 GATGCT 152
Db 235 AGTGCT 240

RESULT 9
US-09-949-016-135525
; Sequence 135525, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; FILE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 135525
; LENGTH: 75929
; TYPE: DNA
; ORGANISM: Human
US-09-949-016-135525
Query Match      20.9%; Score 33.2; DB 3; Length 75929;
Best Local Similarity 54.0%; Pred. No. 3.7;
Matches 68; Conservative 0; Mismatches 58; Indels 0; Gaps 0;

QY 27 CTCAGCTATAAGAGAGCCTCAACCAATGAAATGCTCAACAGCAGCTCAAAAGCTACA 86
Db 31048 CTCAGCCTTCCAAAGTGCCGGGATCACAGGCGTGAACCAACCAACCGCCGACCAAGTTCT 31107

QY 87 GAATCTATTATCAATTTCTGCTCATCTTAATATGCTCTTGTGCTGATCTGTATCATCGT 146
Db 31108 TTTTATATATTTCAGCTCTTCTCATTAATAAACTTTAAAGTTAATGAGCAGTGCTATTGT 31167

QY 147 GATGCT 152
Db 235 AGTGCT 240
```

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; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/100,709
; FILING DATE: 19930729
; CLASSIFICATION: 514
; ATTORNEY/AGENT INFORMATION:
; NAME: Egolf, Christopher
; REGISTRATION NUMBER: 27633
; REFERENCE/DOCKET NUMBER: 7205-49
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 215-757-1590
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 3713 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: circular
; MOLECULE TYPE: DNA (genomic)
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 99..3602
; US-08-100-709-1

Query Match 20.3%; Score 32.2; DB 2; Length 3713;
Best Local Similarity 61.2%; Pred. No. 2.9;
Matches 52; Conservative 0; Mismatches 33; Indels 0; Gaps 0;

QY 73 CGCTAAAGCTACAGAACTCTATTTATCATCTTCTGCTCATCTTAAATATGCTCTTGCTG 132
Db 441 CTTTAAATGCTTCAGCGTATATTTGATAAATTTCTCCCTAATCTTCTTAATTCAGTGATTG 382
QY 133 ATCTGATATCATCGTGCATCTCTCT 157
Db 381 CTTTGTCTTACTGTGCTTCTAT 357

RESULT 13
US-08-176-865-1/c
; Sequence 1, Application US/08176865
; Patent No. 5616319
; GENERAL INFORMATION:
; APPLICANT: Donovan, William P.
; APPLICANT: Tan, Yiping
; APPLICANT: Jany, Christine S.
; APPLICANT: Gonzalez Jr., Jose M.
; TITLE OF INVENTION: BACILLUS THURINGIENSIS cryET4 AND cryET5
; TITLE OF INVENTION: TOXIN GENES AND PROTEINS TOXIC TO LEPIDOPTERAN INSECTS
; NUMBER OF SEQUENCES: 5
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Panitch Schwarze Jacobs & Nadel c/o A.S.
; ADDRESSEE: Nadel
; STREET: 1501 Market Street, 36th Floor
; CITY: Philadelphia
; STATE: Pennsylvania
; COUNTRY: U.S.A.
; ZIP: 19103
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/176,865
; FILING DATE: 30-DEC-1993
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/100,709
; FILING DATE: 29-JUL-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: Egolf, Christopher
; REGISTRATION NUMBER: 27633
; REFERENCE/DOCKET NUMBER: 7205-49

```

Db 31168 AGTGCT 31173

RESULT 11

US-09-949-016-15544

; Sequence 15544, Application US/09949016

; Patent No. 6812339

; GENERAL INFORMATION:

; APPLICANT: VENTER, J. Craig et al.

; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED

; TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF

; FILE REFERENCE: CL0011307

; CURRENT APPLICATION NUMBER: US/09/949,016

; CURRENT FILING DATE: 2000-04-14

; PRIOR APPLICATION NUMBER: 60/241,755

; PRIOR FILING DATE: 2000-10-20

; PRIOR APPLICATION NUMBER: 60/237,768

; PRIOR FILING DATE: 2000-10-03

; PRIOR APPLICATION NUMBER: 60/231,498

; PRIOR FILING DATE: 2000-09-08

; NUMBER OF SEQ ID NOS: 207012

; SOFTWARE: FastSeq for Windows Version 4.0

; SEQ ID NO 15544

; LENGTH: 75929

; TYPE: DNA

; ORGANISM: Human

; FEATURE:

; NAME/KEY: misc.feature

; LOCATION: (1)..(75929)

; OTHER INFORMATION: n = A,T,C or G

US-09-949-016-15544

Query Match 20.9%; Score 33.2; DB 3; Length 75929;

Best Local Similarity 54.0%; Pred. No. 3.7;

Matches 68; Conservative 0; Mismatches 58; Indels 0; Gaps 0;

QY 27 CTCAGCTATTAAGAAGAGCCCTCAACCATTTGAATGCCCTCAACAAGCAGCTCAAAAAGCTACA 86

Db 31048 CTCAGCTTCCAAAGTCCGGGATCATCAGCGTGAACACACACAGCCGACCAACAGTTCT 31107

QY 87 GAATCTATTATCAATTTCTGTCTCATCTTTAAATATGCTCTCTTGCTGATCTGTATCATCTG 146

Db 31108 TTTTATATATTCAGCTCTTCTCTCAATTAATAACTTTAAGTTAATGAGCAGTGCTATTGT 31167

QY 147 GATGCT 152

Db 31168 AGTGCT 31173

RESULT 12

US-08-100-709-1/c

; Sequence 1, Application US/08100709

; Patent No. 5322687

; GENERAL INFORMATION:

; APPLICANT: Donovan, William P.

; APPLICANT: Tan, Yuping

; APPLICANT: Jany, Christine S.

; APPLICANT: Gonzalez Jr., Jose M.

; TITLE OF INVENTION: BACILLUS THURINGIENSIS C1YET4 AND C1YET5

; TITLE OF INVENTION: TOXIN GENES AND PROTEINS TOXIC TO LEPIDOPTERAN INSECTS

; NUMBER OF SEQUENCES: 5

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: Panitch Schwarze Jacobs & Nadel c/o A.S.

; ADDRESSEE: Nadel

; STREET: 1601 Market Street, 36th Floor

; CITY: Philadelphia

; STATE: Pennsylvania

; COUNTRY: U.S.A.

; ZIP: 19103

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk

; COMPUTER: IBM PC compatible

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; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 215-757-1590
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 3713 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: circular
; MOLECULE TYPE: DNA (genomic)
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 99..3602
US-08-176-865-1

Query Match      20.3%; Score 32.2; DB 2; Length 3713;
Best Local Similarity 61.2%; Pred.No.2.9;
Matches 52; Conservative 0; Mismatches 33; Indels 0; Gaps 0;

QY 73 CGTCAAAAGCTACAGAACTATTATCAATTTCTGCTCATCTTAATAATGTCCTTTGCTG 132
DB 441 CTTTAAATGCTTCAGCGTATATTTGATAATTTCTCCCTAACTTCTTAATTCAGTGATTG 382

QY 133 ATCTGTATCATCGTGATGCTTCTCT 157
DB 381 CTTTGTCTTACTGTTGCTTCTAT 357

RESULT 14
US-08-474-038-1/c
; Sequence 1, Application US/08474038
; Patent No. 5679343
; GENERAL INFORMATION:
; APPLICANT: Donovan, William P.
; APPLICANT: Tan, Yuping
; APPLICANT: Jany, Christine S.
; APPLICANT: Gonzalez Jr., Jose M.
; TITLE OF INVENTION: BACILLUS THURINGIENSIS cryET4 AND cryET5
; TITLE OF INVENTION: TOXIN GENES AND PROTEINS TOXIC TO LEPIDOPTERAN INSECTS
; NUMBER OF SEQUENCES: 5
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Panitch Schwarze Jacobs & Nadel c/o A.S.
; ADDRESSEE: Nadel
; STREET: 1601 Market Street, 36th Floor
; CITY: Philadelphia
; STATE: Pennsylvania
; COUNTRY: U.S.A.
; ZIP: 19103
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/474,038
; FILING DATE: 07-JUN-1995
; CLASSIFICATION: 514
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/176,865
; FILING DATE: 30-DEC-1993
; APPLICATION NUMBER: US 08/100,709
; FILING DATE: 29-JUL-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: Egolf, Christopher
; REGISTRATION NUMBER: 27633
; REFERENCE/DOCKET NUMBER: 7205-49
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 215-757-1590
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 3713 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: circular
; MOLECULE TYPE: DNA (genomic)
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 99..3602
US-08-176-865-1

Query Match      20.3%; Score 32.2; DB 2; Length 3713;
Best Local Similarity 61.2%; Pred.No.2.9;
Matches 52; Conservative 0; Mismatches 33; Indels 0; Gaps 0;

QY 73 CGTCAAAAGCTACAGAACTATTATCAATTTCTGCTCATCTTAATAATGTCCTTTGCTG 132
DB 441 CTTTAAATGCTTCAGCGTATATTTGATAATTTCTCCCTAACTTCTTAATTCAGTGATTG 382

QY 133 ATCTGTATCATCGTGATGCTTCTCT 157
DB 381 CTTTGTCTTACTGTTGCTTCTAT 357

RESULT 15
US-08-779-046-1/c
; Sequence 1, Application US/08779046
; Patent No. 5854053
; GENERAL INFORMATION:
; APPLICANT: Donovan, William P.
; APPLICANT: Tan, Yuping
; APPLICANT: Jany, Christine S.
; APPLICANT: Gonzalez Jr., Jose M.
; TITLE OF INVENTION: BACILLUS THURINGIENSIS cryET4 AND cryET5
; TITLE OF INVENTION: TOXIN GENES AND PROTEINS TOXIC TO LEPIDOPTERAN INSECTS
; NUMBER OF SEQUENCES: 5
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Panitch Schwarze Jacobs & Nadel c/o A.S.
; ADDRESSEE: Nadel
; STREET: 1601 Market Street, 36th Floor
; CITY: Philadelphia
; STATE: Pennsylvania
; COUNTRY: U.S.A.
; ZIP: 19103
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/779,046
; FILING DATE: 06-JAN-1997
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/100,709
; FILING DATE: 29-JUL-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: Egolf, Christopher
; REGISTRATION NUMBER: 27633
; REFERENCE/DOCKET NUMBER: 7205-49
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 215-757-1590
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 3713 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: circular
; MOLECULE TYPE: DNA (genomic)
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 99..3602
US-08-779-046-1

Query Match      20.3%; Score 32.2; DB 2; Length 3713;
Best Local Similarity 61.2%; Pred.No.2.9;
Matches 52; Conservative 0; Mismatches 33; Indels 0; Gaps 0;

QY 73 CGTCAAAAGCTACAGAACTATTATCAATTTCTGCTCATCTTAATAATGTCCTTTGCTG 132
DB 441 CTTTAAATGCTTCAGCGTATATTTGATAATTTCTCCCTAACTTCTTAATTCAGTGATTG 382

QY 133 ATCTGTATCATCGTGATGCTTCTCT 157
DB 381 CTTTGTCTTACTGTTGCTTCTAT 357
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QY 73 CGTCAAAAGCTACAGAACTATTATCAATTTCTGTCTCATCTTAATATGTTCTTGTG 132
Db 441 CTTTAAATGCTTCAGCGTATATTGATAATTTCTCCCTAATCTTCTTAATTCAGTGATTG 382
QY 133 ATCTGTATCATCGTGTATGTTCTTCT 157
Db 381 CTTTGGCTTACTGTTGTTCTTCTAT 357

RESULT 16
US-08-881-340-1/c
; Sequence 1, Application US/08881340
; Patent No. 5942658
; GENERAL INFORMATION:
; APPLICANT: Donovan, William P.
; APPLICANT: Tan, Yiping
; APPLICANT: Jany, Christine S.
; APPLICANT: Gonzalez Jr., Jose M.
; TITLE OF INVENTION: BACILLUS THURINGIENSIS cryET4 AND cryET5
; TITLE OF INVENTION: TOXIN GENES AND PROTEINS TOXIC TO LEPIDOPTERAN INSECTS
; NUMBER OF SEQUENCES: 5
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Panitch Schwarze Jacobs & Nadel c/o A.S.
; STREET: 1601 Market Street, 36th Floor
; CITY: Philadelphia
; STATE: Pennsylvania
; COUNTRY: U.S.A.
; ZIP: 19103
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/881.340
; FILING DATE: 24-JUN-1997
; CLASSIFICATION: 424
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/100,709
; FILING DATE: 29-JUL-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: Egolf, Christopher
; REGISTRATION NUMBER: 27633
; REFERENCE/DOCKET NUMBER: 7205-49
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 215-757-1590
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 3713 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: circular
; MOLECULE TYPE: DNA (genomic)
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 99..3602
US-08-881-340-1

Query Match 20.3%; Score 32.2; DB 2; Length 3713;
Best Local Similarity 61.2%; Pred. No. 2.9;
Matches 52; Conservative 0; Mismatches 33; Indels 0; Gaps 0;
QY 73 CGTCAAAAGCTACAGAACTATTATCAATTTCTGTCTCATCTTAATATGTTCTTGTG 132
Db 441 CTTTAAATGCTTCAGCGTATATTGATAATTTCTCCCTAATCTTCTTAATTCAGTGATTG 382
QY 133 ATCTGTATCATCGTGTATGTTCTTCT 157
Db 381 CTTTGGCTTACTGTTGTTCTTCTAT 357

RESULT 17

US-09-949-016-11933/c
; Sequence 11933, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 11933
; LENGTH: 59240
; TYPE: DNA
; ORGANISM: Human
US-09-949-016-11933

Query Match 20.3%; Score 32.2; DB 3; Length 59240;
Best Local Similarity 59.1%; Pred. No. 7;
Matches 55; Conservative 0; Mismatches 38; Indels 0; Gaps 0;
QY 19 CTCACCTCGCTCAGCTATAAGAAGAGCTCAACCACTTGAATGCTCAACAGCAGCTCAA 78
Db 49395 CTCCTTCACACACCTACTAATCAATCAGATCCACATTTAAATATGATCCCGAGTGATTCAT 49336
QY 79 AGCTACAGAATCTATTATCAATTTCTGTCTC 111
Db 49335 AAGCTATTAAAGATATTGTAAAGTTCTATTTC 49303

RESULT 18
US-08-956-171E-283
; Sequence 283, Application US/08956171E
; Patent No. 6593114
; GENERAL INFORMATION:
; APPLICANT: Charles Kunsch
; Gil H. Choi
; Patrick S. Dillon
; Craig A. Rosen
; Steven C. Barash
; Michael R. Fannon
; TITLE OF INVENTION: Staphylococcus aureus Polynucleotides and Sequences
; NUMBER OF SEQUENCES: 5256
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Human Genome Sciences, Inc.
; STREET: 9410 Key West Avenue
; CITY: Rockville
; STATE: Maryland
; COUNTRY: USA
; ZIP: 20850
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette, 3.50 inch, 1.4Mb storage
; COMPUTER: HP Vectra 486/33
; OPERATING SYSTEM: MSDOS version 6.2
; SOFTWARE: ASCII Text
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/956,171E
; FILING DATE: 20-Oct-1997
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 60/009,861
; FILING DATE: January 5, 1996
; APPLICATION NUMBER: 08/781,986
; FILING DATE: January 3, 1997
; ATTORNEY/AGENT INFORMATION:
; NAME: Mark J. Hyman


```

;
;   REGISTRATION NUMBER: 46,789
;   REFERENCE/DOCKET NUMBER: PB248P1
;   TELECOMMUNICATION INFORMATION:
;   TELEPHONE: (240) 314-1224
;   TELEFAX: (301) 309-8439
;   INFORMATION FOR SEQ ID NO: 283:
;   SEQUENCE CHARACTERISTICS:
;   LENGTH: 1421 base pairs
;   TYPE: nucleic acid
;   STRANDEDNESS: double
;   TOPOLOGY: linear
;   SEQUENCE DESCRIPTION: SEQ ID NO: 283:
US-08-956-171E-283

Query Match      20.0%; Score 31.8; DB 3; Length 1421;
Best Local Similarity 61.4%; Pred. No. 2.9; Indels 0; Gaps 0;
Matches 51; Conservative 0; Mismatches 32;

QY 36 AAGAAGAGCCTCAACCATTTGAATGCTCAACAAGCAGCTCAAAAAGCTACAGAAATCTATT 95
DB 317 ACGAAGAAACTGAAATTTTGAATGGTGGTAATCATGTCAAAATATAGTCAAGATGTA 376

QY 96 TATCAATTTCTGCTCATCTTAA 118
DB 377 CTTCATTTACTCTATAAAATAA 399

RESULT 20
US-09-949-016-15725/c
; Sequence 15725, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 15725
; LENGTH: 264358
; TYPE: DNA
; ORGANISM: Human
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (1)-(264358)
; OTHER INFORMATION: n = A,T,C or G
US-09-949-016-15725

Query Match      19.9%; Score 31.6; DB 3; Length 264358;
Best Local Similarity 53.2%; Pred. No. 17; Indels 0; Gaps 0;
Matches 67; Conservative 0; Mismatches 59;

QY 16 TACCTCAGTCGCTCAGCTATTAAGAAGAGCTCAACCATTTGAATGCTCAACAAGCAGCT 75
DB 104340 TACCTTTCTTCCATCTGGCTGAGTAACCTGCCATTCCTTCATGATTAAAGAGG 104281

QY 76 CAAAAGCTACAGAACTATTATCAATTTCTGTCATCTTAATATATGCTCTTGTGCTGATC 135
DB 104280 CAGAAACCTCAGAAATATTTTCTTATTTCTGTCATCTTCTCCCTTTTGAATACC 104221

QY 136 TGTATC 141
DB 104220 AGTTTC 104215

RESULT 21
US-09-949-016-26392/c
; Sequence 26392, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
;

US-08-781-986A-283
; Sequence 283, Application US/08781986A
; Patent No. 6737248
; GENERAL INFORMATION:
; APPLICANT: Charles Kunsch
; TITLE OF INVENTION: Staphylococcus aureus Polynucleotides and Sequences
; NUMBER OF SEQUENCES: 5255
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Human Genome Sciences, Inc.
; STREET: 9410 Key West Avenue
; CITY: Rockville
; STATE: Maryland
; COUNTRY: USA
; ZIP: 20850
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette, 3.50 inch, 1.4Mb storage
; COMPUTER: HP Vectra 486/33
; OPERATING SYSTEM: MSDOS version 6.2
; SOFTWARE: ASCII Text
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/781,986A
; FILING DATE:
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER:
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Benson, Bob
; REGISTRATION NUMBER: 30,446
; REFERENCE/DOCKET NUMBER: PB248PP
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (301) 309-8504
; TELEFAX: (301) 309-8512
; INFORMATION FOR SEQ ID NO: 283:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1421 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: linear
US-08-781-986A-283

Query Match      20.0%; Score 31.8; DB 3; Length 1421;
Best Local Similarity 61.4%; Pred. No. 2.9; Indels 0; Gaps 0;
Matches 51; Conservative 0; Mismatches 32;

QY 36 AAGAAGAGCCTCAACCATTTGAATGCTCAACAAGCAGCTCAAAAAGCTACAGAAATCTATT 95
DB 317 ACGAAGAAACTGAAATTTTGAATGGTGGTAATCATGTCAAAATATAGTCAAGATGTA 376

QY 96 TATCAATTTCTGCTCATCTTAA 118
DB 377 CTTCATTTACTCTATAAAATAA 399
```

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; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 26392
; LENGTH: 601
; TYPE: DNA
; ORGANISM: Human
US-09-949-016-26392

Query Match
Best Local Similarity 19.7%; Score 31.4; DB 3; Length 601;
Matches 56; Conservative 1; Mismatches 42; Indels 0; Gaps 0;

QY 27 CTCAGCTATAGAAGAGCGCTCAACCATTTGAATGCTCAACAGCAGCTCAAAAGCTACA 86
Db 314 CTCGTATTATGTAAGAGATGAATCAGGACTAATAGTAATCTATCTTTGTGAAAGTCTATA 255

QY 87 GAATCTATTTATCAATTTCTGCTCATCTTAATATGCT 125
Db 254 AAATCTATCTTTCTATTCTGTAGTTAATTACATGTTT 216

RESULT 22
US-09-949-016-35374/c
; Sequence 35374, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 35374
; LENGTH: 601
; TYPE: DNA
; ORGANISM: Human
US-09-949-016-35374

Query Match
Best Local Similarity 19.7%; Score 31.4; DB 3; Length 601;
Matches 56; Conservative 1; Mismatches 42; Indels 0; Gaps 0;

QY 27 CTCAGCTATAGAAGAGCGCTCAACCATTTGAATGCTCAACAGCAGCTCAAAAGCTACA 86
Db 314 CTCGTATTATGTAAGAGATGAATCAGGACTAATAGTAATCTATCTTTGTGAAAGTCTATA 255

QY 87 GAATCTATTTATCAATTTCTGCTCATCTTAATATGCT 125
Db 254 AAATCTATCTTTCTATTCTGTAGTTAATTACATGTTT 216

RESULT 23
US-09-949-016-120416/c
; Sequence 120416, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 120416
; LENGTH: 601
; TYPE: DNA
; ORGANISM: Human
US-09-949-016-120416/c

Query Match
Best Local Similarity 19.7%; Score 31.4; DB 3; Length 601;
Matches 56; Conservative 1; Mismatches 42; Indels 0; Gaps 0;

QY 27 CTCAGCTATAGAAGAGCGCTCAACCATTTGAATGCTCAACAGCAGCTCAAAAGCTACA 86
Db 314 CTCGTATTATGTAAGAGATGAATCAGGACTAATAGTAATCTATCTTTGTGAAAGTCTATA 255

QY 87 GAATCTATTTATCAATTTCTGCTCATCTTAATATGCT 125
Db 254 AAATCTATCTTTCTATTCTGTAGTTAATTACATGTTT 216

RESULT 24
US-09-949-016-120420/c
; Sequence 120420, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 120420
; LENGTH: 601
; TYPE: DNA
; ORGANISM: Human
US-09-949-016-120420

Query Match
Best Local Similarity 19.7%; Score 31.4; DB 3; Length 601;
Matches 56; Conservative 1; Mismatches 42; Indels 0; Gaps 0;

QY 27 CTCAGCTATAGAAGAGCGCTCAACCATTTGAATGCTCAACAGCAGCTCAAAAGCTACA 86
Db 314 CTCGTATTATGTAAGAGATGAATCAGGACTAATAGTAATCTATCTTTGTGAAAGTCTATA 255

QY 87 GAATCTATTTATCAATTTCTGCTCATCTTAATATGCT 125
Db 254 AAATCTATCTTTCTATTCTGTAGTTAATTACATGTTT 216

RESULT 25
US-08-439-814-1
; Sequence 1, Application US/08439814
; Patent No. 5968735
; GENERAL INFORMATION:
; APPLICANT: STEIN, Urike
; APPLICANT: WALTHER, Wolfgang
; TITLE OF INVENTION: VECTOR FOR THE EXPRESSION OF
; THERAPY-RELEVANT GENES
; NUMBER OF SEQUENCES: 7
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: NIKAIKO, WARMELSTEIN, MURRAY & ORAM LLP

```

STREET: 655 Fifteenth Street, N. W., Suite 330 G
STREET: Street Lobby
CITY: Washington
STATE: DC
COUNTRY: USA
ZIP: 20005-5701
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/439,814
FILING DATE: 12-MAY-1995
CLASSIFICATION: 514
PRIOR APPLICATION DATA:
APPLICATION NUMBER: DE P 4238778.7
FILING DATE: 12-NOV-1992
APPLICATION NUMBER: DE PCT/DE93/01086
FILING DATE: 10-NOV-1993
ATTORNEY/AGENT INFORMATION:
NAME: KLESNER, Sharon N.
REGISTRATION NUMBER: 36,335
REFERENCE/DOCKET NUMBER: P1614-5015
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202/638-5000
TELEFAX: 202/638-4810
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.30B (EPO)
PRIOR APPLICATION DATA:
APPLICATION NUMBER: DE P4238778.7
FILING DATE: 12-NOV-1992
APPLICATION NUMBER: WO PCT/DE93/01086
FILING DATE: 10-NOV-1993
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 2090 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
US-08-439-814-1

Query Match 19.4%; Score 30.8; DB 2; Length 2090;
Best Local Similarity 63.5%; Pred. No. 6.7; Indels 0; Gaps 0;
Matches 47; Conservative 0; Mismatches 27

QY 86 AGAATCTATTATCAATTTCTGCTCATCTTAATATGCTCTTGCTGATCTGATCATCG 145
Db 112 AGAATCTATTATTTAAATCTGTTATCTTGATCTTTAACTTACTTATATCTTTGATAG 171
QY 146 TGATGCTTCTCTGA 159
Db 172 AGATCTTTACTGA 185

RESULT 26
US-09-949-016-14704
; Sequence 14704, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; PRIORITY FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755

STREET: 655 Fifteenth Street, N. W., Suite 330 G
STREET: Street Lobby
CITY: Washington
STATE: DC
COUNTRY: USA
ZIP: 20005-5701
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/439,814
FILING DATE: 12-MAY-1995
CLASSIFICATION: 514
PRIOR APPLICATION DATA:
APPLICATION NUMBER: DE P 4238778.7
FILING DATE: 12-NOV-1992
APPLICATION NUMBER: DE PCT/DE93/01086
FILING DATE: 10-NOV-1993
ATTORNEY/AGENT INFORMATION:
NAME: KLESNER, Sharon N.
REGISTRATION NUMBER: 36,335
REFERENCE/DOCKET NUMBER: P1614-5015
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202/638-5000
TELEFAX: 202/638-4810
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.30B (EPO)
PRIOR APPLICATION DATA:
APPLICATION NUMBER: DE P4238778.7
FILING DATE: 12-NOV-1992
APPLICATION NUMBER: WO PCT/DE93/01086
FILING DATE: 10-NOV-1993
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 2090 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
US-08-439-814-1

Query Match 19.1%; Score 30.4; DB 3; Length 55061;
Best Local Similarity 57.3%; Pred. No. 25;
Matches 55; Conservative 0; Mismatches 41; Indels 0; Gaps 0;

QY 54 TGAATGCTCTCAACAGCAGCTCAAAAGCTACAGATCTATTATCAATTTCTGCTCAT 113
Db 40347 TAAGTTGCCCAAGAACATTGTGCTATCTAATTAATATATTTTCAATTTGTTTCATT 40406
QY 114 CTTAATATGCTCTTGTGCTGATCTGATCATCGTGAT 149
Db 40407 TTGTTTATACCTTCTTTATCCATTCATATTGAT 40442

RESULT 27
US-09-949-016-14705
; Sequence 14705, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; PRIORITY FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 14705
; LENGTH: 55061
; TYPE: DNA
; ORGANISM: Human
; US-09-949-016-14705

Query Match 19.1%; Score 30.4; DB 3; Length 55061;
Best Local Similarity 57.3%; Pred. No. 25;
Matches 55; Conservative 0; Mismatches 41; Indels 0; Gaps 0;

QY 54 TGAATGCTCTCAACAGCAGCTCAAAAGCTACAGATCTATTATCAATTTCTGCTCAT 113
Db 40347 TAAGTTGCCCAAGAACATTGTGCTATCTAATTAATATATTTTCAATTTGTTTCATT 40406
QY 114 CTTAATATGCTCTTGTGCTGATCTGATCATCGTGAT 149
Db 40407 TTGTTTATACCTTCTTTATCCATTCATATTGAT 40442

RESULT 28
US-09-949-016-14706
; Sequence 14706, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; PRIORITY FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755

; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 14706
; LENGTH: 55061
; TYPE: DNA
; ORGANISM: Human
US-09-949-016-14706

Query Match
Best Local Similarity 19.1%; Score 30.4; DB 3; Length 55061;
Matches 55; Conservative 0; Mismatches 41; Indels 0; Gaps 0;

QY 54 TGAATGCTCAACAGCAGCTCAAAAGCTACAGATCTATTATCAATTTCTGCTCAT 113
DB 40347 TAAGTGGCCCAAGAACATTTGCTATGCTAAATAATATTTTCAATTTGTTTCATT 40406

QY 114 CTTAATATGCTCTTGCTGATCTGTATCATCGTAT 149
DB 40407 TTGTTTATACCTCTTTATCCATTCATATTGAT 40442

RESULT 29
US-09-949-016-14707
; Sequence 14707, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 14707
; LENGTH: 55061
; TYPE: DNA
; ORGANISM: Human
US-09-949-016-14707

Query Match
Best Local Similarity 19.1%; Score 30.4; DB 3; Length 55061;
Matches 55; Conservative 0; Mismatches 41; Indels 0; Gaps 0;

QY 54 TGAATGCTCAACAGCAGCTCAAAAGCTACAGATCTATTATCAATTTCTGCTCAT 113
DB 40347 TAAGTGGCCCAAGAACATTTGCTATGCTAAATAATATTTTCAATTTGTTTCATT 40406

QY 114 CTTAATATGCTCTTGCTGATCTGTATCATCGTAT 149
DB 40407 TTGTTTATACCTCTTTATCCATTCATATTGAT 40442

RESULT 30
US-09-949-016-14708
; Sequence 14708, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.

; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 14708
; LENGTH: 55061
; TYPE: DNA
; ORGANISM: Human
US-09-949-016-14708

Query Match
Best Local Similarity 19.1%; Score 30.4; DB 3; Length 55061;
Matches 55; Conservative 0; Mismatches 41; Indels 0; Gaps 0;

QY 54 TGAATGCTCAACAGCAGCTCAAAAGCTACAGATCTATTATCAATTTCTGCTCAT 113
DB 40347 TAAGTGGCCCAAGAACATTTGCTATGCTAAATAATATTTTCAATTTGTTTCATT 40406

QY 114 CTTAATATGCTCTTGCTGATCTGTATCATCGTAT 149
DB 40407 TTGTTTATACCTCTTTATCCATTCATATTGAT 40442

RESULT 31
US-09-949-016-14709
; Sequence 14709, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 14709
; LENGTH: 55061
; TYPE: DNA
; ORGANISM: Human
US-09-949-016-14709

Query Match
Best Local Similarity 19.1%; Score 30.4; DB 3; Length 55061;
Matches 55; Conservative 0; Mismatches 41; Indels 0; Gaps 0;

QY 54 TGAATGCTCAACAGCAGCTCAAAAGCTACAGATCTATTATCAATTTCTGCTCAT 113
DB 40347 TAAGTGGCCCAAGAACATTTGCTATGCTAAATAATATTTTCAATTTGTTTCATT 40406

QY 114 CTTAATATGCTCTTGCTGATCTGTATCATCGTAT 149
DB 40407 TTGTTTATACCTCTTTATCCATTCATATTGAT 40442

RESULT 32
US-09-949-016-13922
; Sequence 13922, Application US/09949016

Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 13922
; LENGTH: 278866
; TYPE: DNA
; ORGANISM: Human
; FEATURE:
; NAME/KEY: misc.feature
; LOCATION: (1)...(278866)
; OTHER INFORMATION: n = A,T,C or G
US-09-949-016-13922

Query Match 19.1%; Score 30.4; DB 3; Length 278866;
Best Local Similarity 57.3%; Pred. No. 42;
Matches 55; Conservative 0; Mismatches 41; Indels 0; Gaps 0;

QY 54 TGAATGCTCTACAGACGTCACAGAGCTACAGATCTATTATCAATTCGTCTCAT 113
DB 264152 TAAGTTGCCAAGAACATTTGCTATGCTATTAATATATTTTCAATTTGTTTCATTT 264211

QY 114 CTTAATATGTCTCTTCTGCTGATCTGATCATCGTGAT 149
DB 264212 TTGTTTATACCTTCTTTATCCATTCATATTGAT 264247

RESULT 33
US-09-949-016-13923
; Sequence 13923, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 13923
; LENGTH: 278866
; TYPE: DNA
; ORGANISM: Human
; FEATURE:
; NAME/KEY: misc.feature
; LOCATION: (1)...(278866)
; OTHER INFORMATION: n = A,T,C or G
US-09-949-016-13923

Query Match 19.1%; Score 30.4; DB 3; Length 278866;
Best Local Similarity 57.3%; Pred. No. 42;
Matches 55; Conservative 0; Mismatches 41; Indels 0; Gaps 0;

QY 54 TGAATGCTCTACAGACGTCACAGAGCTACAGATCTATTATCAATTCGTCTCAT 113
DB 264152 TAAGTTGCCAAGAACATTTGCTATGCTATTAATATATTTTCAATTTGTTTCATTT 264211

QY 114 CTTAATATGTCTCTTCTGCTGATCTGATCATCGTGAT 149
DB 264212 TTGTTTATACCTTCTTTATCCATTCATATTGAT 264247

RESULT 35
US-09-949-016-13925
; Sequence 13925, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 13925
; LENGTH: 278866
; TYPE: DNA
; ORGANISM: Human

Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 13924
; LENGTH: 278866
; TYPE: DNA
; ORGANISM: Human
; FEATURE:
; NAME/KEY: misc.feature
; LOCATION: (1)...(278866)
; OTHER INFORMATION: n = A,T,C or G
US-09-949-016-13924

Query Match 19.1%; Score 30.4; DB 3; Length 278866;
Best Local Similarity 57.3%; Pred. No. 42;
Matches 55; Conservative 0; Mismatches 41; Indels 0; Gaps 0;

QY 54 TGAATGCTCTACAGACGTCACAGAGCTACAGATCTATTATCAATTCGTCTCAT 113
DB 264152 TAAGTTGCCAAGAACATTTGCTATGCTATTAATATATTTTCAATTTGTTTCATTT 264211

QY 114 CTTAATATGTCTCTTCTGCTGATCTGATCATCGTGAT 149
DB 264212 TTGTTTATACCTTCTTTATCCATTCATATTGAT 264247

RESULT 35
US-09-949-016-13925
; Sequence 13925, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 13925
; LENGTH: 278866
; TYPE: DNA
; ORGANISM: Human

FEATURE: ;
NAME/KEY: misc_feature ;
LOCATION: (1)...(278866) ;
OTHER INFORMATION: n = A,T,C or G ;
US-09-949-016-13925 ;

Query Match 19.1%; Score 30.4; DB 3; Length 278866;
Best Local Similarity 57.3%; Pred. No. 42;
Matches 55; Conservative 0; Mismatches 41; Indels 0; Gaps 0;

QY 54 TGAATGCTCAACAGCAGCTCAAAAGCTACAGATCTATTATCAATTTCTGTCTCAT 113
DB 264152 TAAGTTGCCCAAGAACATTGTGCTATGCTAATTAATATATTTTCAATTTGTTTCATT 264211

QY 114 CTTAATATGCTCTTGTGCTGATCTGTATCATCGTGAT 149
DB 264212 TTGTTTATACCTCTTTTATCCATTCATATTGAT 264247

RESULT 36
US-09-949-016-13926
Sequence 13926, Application US/09949016
Patent No. 6812339
GENERAL INFORMATION:
APPLICANT: VENTER, J. Craig et al.
TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
FILE REFERENCE: CL001307
CURRENT APPLICATION NUMBER: US/09/949,016
CURRENT FILING DATE: 2000-04-14
PRIOR APPLICATION NUMBER: 60/241,755
PRIOR FILING DATE: 2000-10-20
PRIOR APPLICATION NUMBER: 60/237,768
PRIOR FILING DATE: 2000-10-03
PRIOR APPLICATION NUMBER: 60/231,498
PRIOR FILING DATE: 2000-09-08
NUMBER OF SEQ ID NOS: 207012
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 13926
LENGTH: 278866
TYPE: DNA
ORGANISM: Human
FEATURE:
NAME/KEY: misc_feature
LOCATION: (1)...(278866)
OTHER INFORMATION: n = A,T,C or G
US-09-949-016-13926

Query Match 19.1%; Score 30.4; DB 3; Length 278866;
Best Local Similarity 57.3%; Pred. No. 42;
Matches 55; Conservative 0; Mismatches 41; Indels 0; Gaps 0;

QY 54 TGAATGCTCAACAGCAGCTCAAAAGCTACAGATCTATTATCAATTTCTGTCTCAT 113
DB 264152 TAAGTTGCCCAAGAACATTGTGCTATGCTAATTAATATATTTTCAATTTGTTTCATT 264211

QY 114 CTTAATATGCTCTTGTGCTGATCTGTATCATCGTGAT 149
DB 264212 TTGTTTATACCTCTTTTATCCATTCATATTGAT 264247

RESULT 37
US-09-949-016-14699
Sequence 14699, Application US/09949016
Patent No. 6812339
GENERAL INFORMATION:
APPLICANT: VENTER, J. Craig et al.
TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
FILE REFERENCE: CL001307
CURRENT APPLICATION NUMBER: US/09/949,016
CURRENT FILING DATE: 2000-04-14
PRIOR APPLICATION NUMBER: 60/241,755

PRIOR FILING DATE: 2000-10-20
PRIOR APPLICATION NUMBER: 60/237,768
PRIOR FILING DATE: 2000-10-03
PRIOR APPLICATION NUMBER: 60/231,498
PRIOR FILING DATE: 2000-09-08
NUMBER OF SEQ ID NOS: 207012
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 14699
LENGTH: 278866
TYPE: DNA
ORGANISM: Human
FEATURE:
NAME/KEY: misc_feature
LOCATION: (1)...(278866)
OTHER INFORMATION: n = A,T,C or G
US-09-949-016-14699

Query Match 19.1%; Score 30.4; DB 3; Length 278866;
Best Local Similarity 57.3%; Pred. No. 42;
Matches 55; Conservative 0; Mismatches 41; Indels 0; Gaps 0;

QY 54 TGAATGCTCAACAGCAGCTCAAAAGCTACAGATCTATTATCAATTTCTGTCTCAT 113
DB 264152 TAAGTTGCCCAAGAACATTGTGCTATGCTAATTAATATATTTTCAATTTGTTTCATT 264211

QY 114 CTTAATATGCTCTTGTGCTGATCTGTATCATCGTGAT 149
DB 264212 TTGTTTATACCTCTTTTATCCATTCATATTGAT 264247

RESULT 38
US-09-949-016-14700
Sequence 14700, Application US/09949016
Patent No. 6812339
GENERAL INFORMATION:
APPLICANT: VENTER, J. Craig et al.
TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
FILE REFERENCE: CL001307
CURRENT APPLICATION NUMBER: US/09/949,016
CURRENT FILING DATE: 2000-04-14
PRIOR APPLICATION NUMBER: 60/241,755
PRIOR FILING DATE: 2000-10-20
PRIOR APPLICATION NUMBER: 60/237,768
PRIOR FILING DATE: 2000-10-03
PRIOR APPLICATION NUMBER: 60/231,498
PRIOR FILING DATE: 2000-09-08
NUMBER OF SEQ ID NOS: 207012
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 14700
LENGTH: 278866
TYPE: DNA
ORGANISM: Human
FEATURE:
NAME/KEY: misc_feature
LOCATION: (1)...(278866)
OTHER INFORMATION: n = A,T,C or G
US-09-949-016-14700

Query Match 19.1%; Score 30.4; DB 3; Length 278866;
Best Local Similarity 57.3%; Pred. No. 42;
Matches 55; Conservative 0; Mismatches 41; Indels 0; Gaps 0;

QY 54 TGAATGCTCAACAGCAGCTCAAAAGCTACAGATCTATTATCAATTTCTGTCTCAT 113
DB 264152 TAAGTTGCCCAAGAACATTGTGCTATGCTAATTAATATATTTTCAATTTGTTTCATT 264211

QY 114 CTTAATATGCTCTTGTGCTGATCTGTATCATCGTGAT 149
DB 264212 TTGTTTATACCTCTTTTATCCATTCATATTGAT 264247

RESULT 39

```
US-09-949-016-14701
; Sequence 14701, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 14701
; LENGTH: 278866
; TYPE: DNA
; ORGANISM: Human
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (1)..(278866)
; OTHER INFORMATION: n = A,T,C or G
US-09-949-016-14701

Query Match          19.1%; Score 30.4; DB 3; Length 278866;
Best Local Similarity 57.3%; Pred. No. 42;
Matches 55; Conservative 0; Mismatches 41; Indels 0; Gaps 0;

QY      54  TGAATGCTCAACAGCAGCTCAAGAGCTACAGATCTATTATCAATTTCTGTCTCAT 113
Db      264152  TAAGTTGCCAAGAACAATGTGCTATGCTAATAATAATATTTTCAATTTGTTTCATTT 264211

QY      114  CTTAATATGCTCTTCTGCTGATCTGTATCATCGTGAT 149
Db      264212  TTGTTTATACCCCTCTTTATCCATCCATATGAT 264247

RESULT 41
US-09-949-016-14703
; Sequence 14703, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 14703
; LENGTH: 278866
; TYPE: DNA
; ORGANISM: Human
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (1)..(278866)
; OTHER INFORMATION: n = A,T,C or G
US-09-949-016-14703

Query Match          19.1%; Score 30.4; DB 3; Length 278866;
Best Local Similarity 57.3%; Pred. No. 42;
Matches 55; Conservative 0; Mismatches 41; Indels 0; Gaps 0;

QY      54  TGAATGCTCAACAGCAGCTCAAGAGCTACAGATCTATTATCAATTTCTGTCTCAT 113
Db      264152  TAAGTTGCCAAGAACAATGTGCTATGCTAATAATAATATTTTCAATTTGTTTCATTT 264211

QY      114  CTTAATATGCTCTTCTGCTGATCTGTATCATCGTGAT 149
Db      264212  TTGTTTATACCCCTCTTTATCCATCCATATGAT 264247

RESULT 42
US-09-949-016-15088
; Sequence 15088, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 15088
; LENGTH: 9811
; TYPE: DNA
; ORGANISM: Human
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (1)..(278866)
; OTHER INFORMATION: n = A,T,C or G
US-09-949-016-14702

Query Match          19.1%; Score 30.4; DB 3; Length 278866;
Best Local Similarity 57.3%; Pred. No. 42;
Matches 55; Conservative 0; Mismatches 41; Indels 0; Gaps 0;

QY      54  TGAATGCTCAACAGCAGCTCAAGAGCTACAGATCTATTATCAATTTCTGTCTCAT 113
Db      264152  TAAGTTGCCAAGAACAATGTGCTATGCTAATAATAATATTTTCAATTTGTTTCATTT 264211

QY      114  CTTAATATGCTCTTCTGCTGATCTGTATCATCGTGAT 149
Db      264212  TTGTTTATACCCCTCTTTATCCATCCATATGAT 264247

RESULT 40
US-09-949-016-14702
; Sequence 14702, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 14702
; LENGTH: 278866
; TYPE: DNA
; ORGANISM: Human
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (1)..(278866)
; OTHER INFORMATION: n = A,T,C or G
US-09-949-016-14702

Query Match          19.1%; Score 30.4; DB 3; Length 278866;
Best Local Similarity 57.3%; Pred. No. 42;
Matches 55; Conservative 0; Mismatches 41; Indels 0; Gaps 0;
```



```
; TYPE: DNA
; ORGANISM: Human
US-09-949-016-15088

Query Match      19.0%; Score 30.2; DB 3; Length 9811;
Best Local Similarity 56.6%; Pred. No. 17;
Matches 56; Conservative 0; Mismatches 43; Indels 0; Gaps 0;

QY 27 CTCAGCTATAAGAGAGCGCTCAACCAATTCGCTCAACAGCAGCTCAAAAGCTACA 86
DB 4316 CTCTGTTATGTGACAAGATGAATCAGGACTAATAGTAACTATCTTGTGAAAGTCTATA 4375

QY 87 GAATCTATTATCAATTTCTCTCATCTTAATATGCTT 125
DB 4376 AAATCTATCTTTCTATTTCTGTAGTTAATTACATGTTT 4414

RESULT 43
US-09-949-016-15089
; Sequence 15089, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 15089
; LENGTH: 9811
; TYPE: DNA
; ORGANISM: Human
US-09-949-016-15089

Query Match      19.0%; Score 30.2; DB 3; Length 9811;
Best Local Similarity 56.6%; Pred. No. 17;
Matches 56; Conservative 0; Mismatches 43; Indels 0; Gaps 0;

QY 27 CTCAGCTATAAGAGAGCGCTCAACCAATTCGCTCAACAGCAGCTCAAAAGCTACA 86
DB 4316 CTCTGTTATGTGACAAGATGAATCAGGACTAATAGTAACTATCTTGTGAAAGTCTATA 4375

QY 87 GAATCTATTATCAATTTCTCTCATCTTAATATGCTT 125
DB 4376 AAATCTATCTTTCTATTTCTGTAGTTAATTACATGTTT 4414

RESULT 44
US-09-949-016-12176
; Sequence 12176, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 12176
; LENGTH: 9864
; TYPE: DNA
; ORGANISM: Human
US-09-949-016-12176

Query Match      19.0%; Score 30.2; DB 3; Length 9964;
Best Local Similarity 56.6%; Pred. No. 17;
Matches 56; Conservative 0; Mismatches 43; Indels 0; Gaps 0;

QY 27 CTCAGCTATAAGAGAGCGCTCAACCAATTCGCTCAACAGCAGCTCAAAAGCTACA 86
DB 4472 CTCTGTTATGTGACAAGATGAATCAGGACTAATAGTAACTATCTTGTGAAAGTCTATA 4531

QY 87 GAATCTATTATCAATTTCTCTCATCTTAATATGCTT 125
DB 4532 AAATCTATCTTTCTATTTCTGTAGTTAATTACATGTTT 4570

RESULT 45
US-09-949-016-12685
; Sequence 12685, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 12685
; LENGTH: 16190
; TYPE: DNA
; ORGANISM: Human
US-09-949-016-12685

Query Match      19.0%; Score 30.2; DB 3; Length 16190;
Best Local Similarity 60.2%; Pred. No. 41;
Matches 50; Conservative 0; Mismatches 33; Indels 0; Gaps 0;

QY 23 CTGCTCAGCTATAAGAGAGCGCTCAACCAATTCGCTCAACAGCAGCTCAAAAGC 82
DB 161769 CTCTCTTGGCATCTGCTCAGCTAAACCAATGAATGCGTTTACATCAGACTAAACA 161828

QY 83 TACAGAACTATTATCAATTTC 105
DB 161829 AACAAACACTTTGTAGGTATATC 161851

RESULT 46
US-09-949-016-12906
; Sequence 12906, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
```

; TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 12906
; LENGTH: 161914
; TYPE: DNA
; ORGANISM: Human
; FEATURE:
; NAME/KEY: misc.feature
; LOCATION: (1)...(161914)
; OTHER INFORMATION: n = A,T,C or G
US-09-949-016-12906

Query Match 19.0%; Score 30.2; DB 3; Length 161914;
Best Local Similarity 60.2%; Pred. No. 41;
Matches 50; Conservative 0; Mismatches 33; Indels 0; Gaps 0;

QY 23 CTCGCTCAGCTATAAGAGAGCTCAACCAATTCGAATGCTCAACAGCAGCTCAAAAGC 82
Db 161779 CTCCTTCCATCTCTCAGCCTCAACCAATGAATGGCTTTACAATCAGACTAAACA 161838

QY 83 TACAGAATCTATTATCAATTC 105
Db 161839 AACAAACACTTTAGGTATATC 161861

RESULT 47
US-09-949-016-196215/c
; Sequence 196215, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 196215
; LENGTH: 601
; TYPE: DNA
; ORGANISM: Human
US-09-949-016-196215

Query Match 18.9%; Score 30; DB 3; Length 601;
Best Local Similarity 52.4%; Pred. No. 8;
Matches 66; Conservative 0; Mismatches 60; Indels 0; Gaps 0;

QY 23 CTCGCTCAGCTATAAGAGAGCTCAACCAATTCGAATGCTCAACAGCAGCTCAAAAGC 82
Db 446 CTGCTCAGCTCTCTGAATAGCTGGACTATATATGCACACCACTGCTGGCTAATTA 387

QY 83 TACAGAATCTATTATCAATTC 105
Db 386 CTTTATTATTTATTTATTTATTTATTTATTTATTTATTTATTTATTTATTTATTTT 327
QY 143 TCGTGA 148

Db 326 TTTTGA 321

RESULT 48
US-08-998-416-295/c
; Sequence 295, Application US/08998416
; Patent No. 6239264
; GENERAL INFORMATION:
; APPLICANT: Philippaen, Peter
; APPLICANT: Pohlmann, Rainer
; APPLICANT: Steiner, Sabine
; APPLICANT: Mohr, Christine
; APPLICANT: Wendland, Jurgen
; APPLICANT: Knechtle, Philipp
; APPLICANT: Rebischung, Corinne
; TITLE OF INVENTION: GENOMIC DNA SEQUENCES OF ASHBYA GOSSYPHII
; TITLE OF INVENTION: AND USES THEREOF
; NUMBER OF SEQUENCES: 1152
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: No. 6239264artis Corporation
; STREET: 3054 Cornwallis Road
; CITY: Research Triangle Park
; STATE: No. 6239264th Carolina
; COUNTRY: USA
; ZIP: 27709
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/998,416
; FILING DATE: 24-DEC-1997
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: CH 0016/97
; FILING DATE: 31-DEC-1996
; ATTORNEY/AGENT INFORMATION:
; NAME: Meigs, J. Timothy
; REGISTRATION NUMBER: 38,241
; REFERENCE/DOCKET NUMBER: PF/5-30306/A/CGC1976
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 919-541-8587
; TELEFAX: 919-541-8689
; INFORMATION FOR SEQ ID NO: 295:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 859 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
; ORIGINAL SOURCE:
; ORGANISM: PAG1244UP
; US-08-998-416-295

Query Match 18.9%; Score 30; DB 3; Length 859;
Best Local Similarity 53.4%; Pred. No. 9;
Matches 63; Conservative 0; Mismatches 55; Indels 0; Gaps 0;

QY 16 TACCTCAGCTCAGCTATATAAGAGAGCTCAACCAATTCGAATGCTCAACAGCAGCT 75
Db 489 TGCTTAAATGGTCACCAGCCTAGTGGCCGCTGTTATGATATATATATATATATG 430

QY 76 CAAAAGCTACAGATCTATTATCAATTTCTGCTCATCTTAATATCTCTCTTCTGCTGA 133
Db 429 CATACGCACTGAAGCTAGTTGCAAGTTTGGCTCTCTTATATATATATATCTTAGGAGA 372

RESULT 49
US-09-949-016-12542
; Sequence 12542, Application US/09949016
; Patent No. 6812339

GENERAL INFORMATION:
APPLICANT: VENTER, J. Craig et al.
TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
FILE REFERENCE: CL001307
CURRENT APPLICATION NUMBER: US/09/949,016
CURRENT FILING DATE: 2000-04-14
PRIOR APPLICATION NUMBER: 60/241,755
PRIOR FILING DATE: 2000-10-20
PRIOR APPLICATION NUMBER: 60/237,768
PRIOR FILING DATE: 2000-10-03
PRIOR APPLICATION NUMBER: 60/231,498
PRIOR FILING DATE: 2000-09-08
NUMBER OF SEQ ID NOS: 207012
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 12542
LENGTH: 173787
TYPE: DNA
ORGANISM: Human
US-09-949-016-12542

Query Match 18.9%; Score 30; DB 3; Length 173787;
Best Local Similarity 52.4%; Pred. No. 48;
Matches 66; Conservative 0; Mismatches 60; Indels 0; Gaps 0;
Qy 23 CTCGCTCAGCTATAGAAGAGCCTCAACCAATGCTCAACAGCAGTCAAAAGC 82
Db 72869 CTGCTCAGCTCTCTGAATAGCTGGACTATATATGACACACCATGCGCTAATTA 72928
Qy 83 TACAGAACTATTATCAATTTCTGTCATCTTAATATGTCCTGCTGATCTGTATCA 142
Db 72929 CTTTATTATTATTATTATTATTATTATTATTATTATTATTATTATTATTATT 72988
Qy 143 TCGTGA 148
Db 72989 TTTTGA 72994

RESULT 50
US-09-949-016-17302
Sequence 17302, Application US/09949016
Patent No. 6812339
GENERAL INFORMATION:
APPLICANT: VENTER, J. Craig et al.
TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
FILE REFERENCE: CL001307
CURRENT APPLICATION NUMBER: US/09/949,016
CURRENT FILING DATE: 2000-04-14
PRIOR APPLICATION NUMBER: 60/241,755
PRIOR FILING DATE: 2000-10-20
PRIOR APPLICATION NUMBER: 60/237,768
PRIOR FILING DATE: 2000-10-03
PRIOR APPLICATION NUMBER: 60/231,498
PRIOR FILING DATE: 2000-09-08
NUMBER OF SEQ ID NOS: 207012
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 17302
LENGTH: 173791
TYPE: DNA
ORGANISM: Human
US-09-949-016-17302

Query Match 18.9%; Score 30; DB 3; Length 173791;
Best Local Similarity 52.4%; Pred. No. 48;
Matches 66; Conservative 0; Mismatches 60; Indels 0; Gaps 0;
Qy 23 CTCGCTCAGCTATAGAAGAGCCTCAACCAATGCTCAACAGCAGTCAAAAGC 82
Db 72869 CTGCTCAGCTCTCTGAATAGCTGGACTATATATGACACACCATGCGCTAATTA 72928
Qy 83 TACAGAACTATTATCAATTTCTGTCATCTTAATATGTCCTGCTGATCTGTATCA 142

Db 72929 CTTTATTATTATTATTATTATTATTATTATTATTATTATTATTATTATTATT 72988
Qy 143 TCGTGA 148
Db 72989 TTTTGA 72994
Search completed: December 8, 2005, 02:16:30
Job time : 147 secs

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OM nucleic - nucleic search, using sw model

Run On: December 8, 2005, 01:11:35 ; Search time 809 Seconds

(without alignments)
1625.255 Million cell updates/sec

Title: US-10-691-412-1

Perfect score: 159

Sequence: 1 atggagaaagtcataact.....tcacgtgatgtctctga 159

Scoring table: IDENTITY_NUC

Gapop 10.0 , Gapext 1.0

Searched: 9793542 seqs, 4134689005 residues

Total number of hits satisfying chosen parameters: 19587084

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 100 summaries

Database : Published Applications NA_Main:

- 1: /cgn2_6/ptodata/1/pubpna/US07_PUBCOMB.seq*
- 2: /cgn2_6/ptodata/1/pubpna/US08_PUBCOMB.seq*
- 3: /cgn2_6/ptodata/1/pubpna/US09_PUBCOMB.seq*
- 4: /cgn2_6/ptodata/1/pubpna/US09B_PUBCOMB.seq*
- 5: /cgn2_6/ptodata/1/pubpna/US10A_PUBCOMB.seq*
- 6: /cgn2_6/ptodata/1/pubpna/US10B_PUBCOMB.seq*
- 7: /cgn2_6/ptodata/1/pubpna/US10C_PUBCOMB.seq*
- 8: /cgn2_6/ptodata/1/pubpna/US10D_PUBCOMB.seq*
- 9: /cgn2_6/ptodata/1/pubpna/US10E_PUBCOMB.seq*
- 10: /cgn2_6/ptodata/1/pubpna/US11_PUBCOMB.seq*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	159	100.0	159	8	US-10-691-412-1
2	159	100.0	525	3	US-09-918-995-4045
3	159	100.0	1635	3	US-09-873-367C-162
4	159	100.0	1635	9	US-10-843-641A-162
5	159	100.0	1712	10	US-11-019-855-1
6	158	99.4	380	3	US-09-918-995-1950
7	158	99.4	418	3	US-09-918-995-5235
8	157.4	99.0	334	3	US-09-918-995-4217
9	147.8	93.0	487	3	US-09-918-995-5377
10	147.8	93.0	492	3	US-09-918-995-17377
11	144.6	90.9	159	6	US-10-371-101-13
12	144.6	90.9	407	3	US-09-918-995-3842
13	143	89.9	159	6	US-10-371-101-9
14	83	52.2	315	8	US-10-815-514-26
15	83	52.2	315	8	US-10-877-930-26
16	83	52.2	315	9	US-10-873-594-26
17	46	28.9	108	8	US-10-724-532-3
18	46	28.9	108	8	US-10-724-532-4
19	46	28.9	135	8	US-10-724-532-5
20	46	28.9	135	8	US-10-724-532-6
21	34.2	21.5	589	4	US-09-925-065A-575150
22	34.2	21.5	589	4	US-09-925-065A-575151
23	34.2	21.5	786452	8	US-10-719-993-6822
					Sequence 1, Appli
					Sequence 4045, Ap
					Sequence 162, App
					Sequence 162, App
					Sequence 1, Appli
					Sequence 3950, Ap
					Sequence 5235, Ap
					Sequence 4217, Ap
					Sequence 5377, Ap
					Sequence 13, Appl
					Sequence 3842, Ap
					Sequence 9, Appli
					Sequence 26, Appl
					Sequence 26, Appl
					Sequence 26, Appl
					Sequence 3, Appli
					Sequence 4, Appli
					Sequence 5, Appli
					Sequence 6, Appli
					Sequence 575150,
					Sequence 6822, Ap

33.4	21.0	37973	6	US-10-311-455-2169	Sequence 2169, Ap
33.2	20.9	201	8	US-10-719-993-26457	Sequence 26457, A
32.6	20.5	170279	8	US-10-388-838-1	Sequence 1, Appli
32.2	20.3	402	10	US-11-029-984-845	Sequence 845, App
32	20.1	451	4	US-09-925-065A-150093	Sequence 150093,
31.8	20.0	359	5	US-10-027-632-140279	Sequence 140279,
31.8	20.0	359	5	US-10-027-632-140279	Sequence 140279,
31.8	20.0	636	4	US-09-925-065A-536994	Sequence 536994,
31.8	20.0	1421	2	US-08-781-986A-283	Sequence 283, App
31.8	20.0	1421	2	US-10-329-624-283	Sequence 283, App
31.8	20.0	6025	8	US-10-857-625-76	Sequence 76, Appl
31.6	19.9	812	4	US-09-925-065A-179738	Sequence 179738,
31.4	19.7	519	4	US-09-925-065A-255686	Sequence 255686,
31.4	19.7	519	4	US-09-925-065A-255687	Sequence 255687,
31.4	19.7	560	4	US-09-925-065A-246839	Sequence 246839,
31.4	19.7	873	9	US-10-450-763-5048	Sequence 5048, Ap
31.4	19.7	873	9	US-10-450-763-5355	Sequence 5355, Ap
31.4	19.7	873	9	US-10-450-763-11273	Sequence 11273, A
31.4	19.7	1199	7	US-10-437-963-88801	Sequence 88801, A
31.4	19.7	3505	10	US-11-097-143-27115	Sequence 27115, A
31.4	19.7	5875	6	US-10-311-455-261	Sequence 261, App
31.4	19.7	2940917	5	US-10-027-632-174763	Sequence 174763,
31.4	19.7	2940917	6	US-10-027-632-174763	Sequence 174763,
31.2	19.6	453	7	US-10-424-599-49155	Sequence 49155, A
31.2	19.6	84073	5	US-10-087-192-712	Sequence 712, App
31.2	19.5	633	5	US-10-027-632-233567	Sequence 233567,
31	19.5	633	6	US-10-027-632-233567	Sequence 233567,
31	19.5	663	8	US-10-425-115-47211	Sequence 47211, A
31	19.5	1269	8	US-10-767-795-1475	Sequence 1475, Ap
31	19.5	2162	7	US-10-437-963-18523	Sequence 18523, A
31	19.5	5206	7	US-10-437-963-77914	Sequence 77914, A
31	19.5	6182	6	US-10-311-455-1988	Sequence 87, Appl
31	19.5	271990	6	US-10-195-144-87	Sequence 87, Appl
31	19.5	271990	6	US-10-345-072-87	Sequence 87, Appl
30.8	19.4	309	5	US-10-027-632-264616	Sequence 264616,
30.8	19.4	309	5	US-10-027-632-264617	Sequence 264617,
30.8	19.4	309	6	US-10-027-632-264617	Sequence 264617,
30.8	19.4	437	8	US-10-767-795-1993	Sequence 1993, Ap
30.8	19.4	524	4	US-09-925-065A-418006	Sequence 418006,
30.8	19.4	739	4	US-09-925-065A-85147	Sequence 85147, A
30.8	19.4	10200	9	US-10-415-607-5	Sequence 5, Appli
30.8	19.4	177380	8	US-10-484-577-683	Sequence 683, App
30.6	19.2	336	4	US-09-925-065A-143336	Sequence 143336,
30.6	19.2	349	3	US-09-960-352-1428	Sequence 1428, Ap
30.6	19.2	426	8	US-10-674-124A-2911	Sequence 2911, Ap
30.6	19.2	442	4	US-09-925-065A-644502	Sequence 644502, A
30.6	19.2	496	3	US-09-918-995-25194	Sequence 25194, A
30.6	19.2	541	4	US-09-925-065A-216894	Sequence 216894,
30.6	19.2	551	3	US-09-867-701-6051	Sequence 6051, Ap
30.6	19.2	596	4	US-09-925-065A-302480	Sequence 302480,
30.6	19.2	607	4	US-09-925-065A-655605	Sequence 655605,
30.6	19.2	930	7	US-10-220-120-9	Sequence 9, Appli
30.6	19.2	1132	5	US-10-103-313-67	Sequence 67, Appl
30.6	19.2	1592	9	US-10-756-149-180	Sequence 180, App
30.6	19.2	1973	3	US-09-814-353-20163	Sequence 20163, A
30.6	19.2	89873	9	US-10-461-862-61	Sequence 61, Appl
30.6	19.2	95109	7	US-10-433-287-80	Sequence 80, Appl
30.4	19.1	542	4	US-09-925-065A-828136	Sequence 828136,
30.4	19.1	561	4	US-09-925-065A-828135	Sequence 828135,
30.4	19.1	563	4	US-09-925-065A-828135	Sequence 828135,
30.4	19.1	570	4	US-09-925-065A-828142	Sequence 828142,
30.4	19.1	604	4	US-09-925-065A-832584	Sequence 832584,
30.4	19.1	614	4	US-09-925-065A-750309	Sequence 750309,
30.4	19.1	614	4	US-09-925-065A-750310	Sequence 750310,
30.4	19.1	614	4	US-09-925-065A-822696	Sequence 822696,
30.2	19.0	248	8	US-10-674-124A-8992	Sequence 8992, Ap
30.2	19.0	277	3	US-09-294-093B-2256	Sequence 2256, Ap
30.2	19.0	433	5	US-10-027-632-140644	Sequence 140644,
30.2	19.0	433	5	US-10-027-632-140645	Sequence 140645,
30.2	19.0	433	6	US-10-027-632-140645	Sequence 140645,
30.2	19.0	433	6	US-10-027-632-140645	Sequence 803161,

97 30.2 19.0 612 8 US-10-357-930-6502 Sequence 6502, Ap
c 98 30.2 19.0 1044 5 US-10-027-632-100666 Sequence 100666,
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c 100 30.2 19.0 1446 8 US-10-425-115-129555 Sequence 129555,

ALIGNMENTS

RESULT 1
US-10-691-412-1
; Sequence 1, Application US/10691412
; Publication No. US20040191802A1
; GENERAL INFORMATION:
; APPLICANT: Kranias, Evangelia G.
; APPLICANT: Kobra, Haghighi
; TITLE OF INVENTION: Phospholamban Polymorphisms and Methods of Assessment
; FILE REFERENCE: 10738-47
; CURRENT APPLICATION NUMBER: US/10/691,412
; CURRENT FILING DATE: 2003-10-22
; NUMBER OF SEQ ID NOS: 6
; SOFTWARE: Patent in version 3.2
; SEQ ID NO 1
; LENGTH: 159
; TYPE: DNA
; ORGANISM: Human
US-10-691-412-1

Query Match 100.0%; Score 159; DB 8; Length 159;
Best Local Similarity 100.0%; Pred. No. 1.6e-37;
Matches 159; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ATGGAGAAAGTCCAATACCTCAGCTATATAAGAGAGCGCTCAACCATTTGAATG 60
Db 1 ATGGAGAAAGTCCAATACCTCAGCTATATAAGAGAGCGCTCAACCATTTGAATG 60

QY 61 CCTCAACAGCAGCTCAAAAGCTACAGAATCTATTATCAATTTCTGTCTCATCTTAATA 120
Db 61 CCTCAACAGCAGCTCAAAAGCTACAGAATCTATTATCAATTTCTGTCTCATCTTAATA 120

QY 121 TGTCTCTTGTGATCTGTATCATCGTGATGCTTCTCTGA 159
Db 121 TGTCTCTTGTGATCTGTATCATCGTGATGCTTCTCTGA 468

RESULT 2
US-09-873-367C-162
; Sequence 162, Application US/09873367C
; Publication No. US20030165839A1
; GENERAL INFORMATION:
; APPLICANT: Young, Paul
; APPLICANT: Soppet, Daniel
; APPLICANT: Endress, Gregory
; APPLICANT: Augustus, Meena
; APPLICANT: Ebner, Reinhard
; APPLICANT: Carter, Kenneth
; TITLE OF INVENTION: Cancer Gene Determination and Therapeutic Screening Using
; FILE REFERENCE: 689290-64
; CURRENT APPLICATION NUMBER: US/09/873,367C
; CURRENT FILING DATE: 2003-04-29
; PRIOR APPLICATION NUMBER: U.S. 60/236,891
; PRIOR FILING DATE: 2000-09-29
; PRIOR APPLICATION NUMBER: U.S. 60/236,842
; PRIOR FILING DATE: 2000-09-29
; PRIOR APPLICATION NUMBER: U.S. 60/244,867
; PRIOR FILING DATE: 2000-11-01
; PRIOR APPLICATION NUMBER: U.S. 60/245,084
; PRIOR FILING DATE: 2000-11-01
; NUMBER OF SEQ ID NOS: 1067
; SOFTWARE: Patent in version 3.0
; SEQ ID NO 162
; LENGTH: 1635
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-873-367C-162

Query Match 100.0%; Score 159; DB 3; Length 1635;
Best Local Similarity 100.0%; Pred. No. 4.2e-37;
Matches 159; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ATGGAGAAAGTCCAATACCTCAGCTATATAAGAGAGCGCTCAACCATTTGAATG 60
Db 182 ATGGAGAAAGTCCAATACCTCAGCTATATAAGAGAGCGCTCAACCATTTGAATG 241

QY 61 CCTCAACAGCAGCTCAAAAGCTACAGAATCTATTATCAATTTCTGTCTCATCTTAATA 120
Db 242 CCTCAACAGCAGCTCAAAAGCTACAGAATCTATTATCAATTTCTGTCTCATCTTAATA 301

QY 121 TGTCTCTTGTGATCTGTATCATCGTGATGCTTCTCTGA 159
Db 302 TGTCTCTTGTGATCTGTATCATCGTGATGCTTCTCTGA 340

RESULT 3
US-10-843-641A-162
; Sequence 162, Application US/10843641A
; Publication No. US20050064454A1
; GENERAL INFORMATION:
; APPLICANT: Avalon Pharmaceuticals, Inc.
; APPLICANT: Cancer Gene Determination and Therapeutic Screening Using
; TITLE OF INVENTION: Signature Gene Sets
; FILE REFERENCE: 689290-189
; CURRENT APPLICATION NUMBER: US/10/843,641A
US-10-843-641A-162

Query Match 100.0%; Score 159; DB 3; Length 525;
Best Local Similarity 100.0%; Pred. No. 2.6e-37;
Matches 159; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ATGGAGAAAGTCCAATACCTCAGCTATATAAGAGAGCGCTCAACCATTTGAATG 60
Db 1 ATGGAGAAAGTCCAATACCTCAGCTATATAAGAGAGCGCTCAACCATTTGAATG 60

QY 61 CCTCAACAGCAGCTCAAAAGCTACAGAATCTATTATCAATTTCTGTCTCATCTTAATA 120
Db 61 CCTCAACAGCAGCTCAAAAGCTACAGAATCTATTATCAATTTCTGTCTCATCTTAATA 120

QY 121 TGTCTCTTGTGATCTGTATCATCGTGATGCTTCTCTGA 159
Db 121 TGTCTCTTGTGATCTGTATCATCGTGATGCTTCTCTGA 159

RESULT 4
US-09-918-995-4045
; Sequence 4045, Application US/09918995
; Publication No. US20030073623A1
; GENERAL INFORMATION:
; APPLICANT: Hyseq, Inc.
; TITLE OF INVENTION: NOVEL NUCLEIC ACID SEQUENCES OBTAINED
; TITLE OF INVENTION: FROM VARIOUS CDNA LIBRARIES
; FILE REFERENCE: 20411-756
; CURRENT APPLICATION NUMBER: US/09/918,995
; CURRENT FILING DATE: 2001-07-30
; PRIOR APPLICATION NUMBER: US/09/235,076
; PRIOR FILING DATE: 1999-01-20
; NUMBER OF SEQ ID NOS: 38054
; SOFTWARE: Fast-Seq for Windows Version 3.0
; SEQ ID NO 4045
; LENGTH: 525
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (1)-(525)
; OTHER INFORMATION: n = A,T,C or G
US-09-918-995-4045

Query Match 100.0%; Score 159; DB 3; Length 525;
Best Local Similarity 100.0%; Pred. No. 2.6e-37;
Matches 159; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

	Qy	1	ATGGAGAAAGTCCAATACTCACTCGCTCAGCTATAAGAAGAGGCTCAACCATTTCAAATG	60
	Db	182	ATGGAGAAAGTCCAATACTCACTCGCTCAGCTATAAGAAGAGGCTCAACCATTTCAAATG	241
	Qy	61	CCTCAACAAGCACGCTCAAAAAGCTACAGAATCTATTATTCATTTCTGTCTCATCTTAATA	120
	Db	242	CCTCAACAAGCACGCTCAAAAAGCTACAGAATCTATTATCAATTTCTGTCTCATCTTAATA	301
	Qy	121	TGTCCTTGCTGATCTGTATCATCTGATGCTTCTCTGA	159
	Db	302	TGTCCTTGCTGATCTGTATCATCTGATGCTTCTCTGA	340
		RESULT 6		
		US-09-918-995-3950		
		; Sequence 3950, Application US/09918995		
		; Publication No. US20030073623A1		
		; GENERAL INFORMATION:		
		; APPLICANT: Hyseq, Inc.		
		; TITLE OF INVENTION: NOVEL NUCLEIC ACID SEQUENCES OBTAINED		
		; FILE REFERENCE: 20411-756		
		; CURRENT APPLICATION NUMBER: US/09/918,995		
		; CURRENT FILING DATE: 2001-07-30		
		; PRIOR APPLICATION NUMBER: US/09/235,076		
		; PRIOR FILING DATE: 1999-01-20		
		; NUMBER OF SEQ ID NOS: 38054		
		; SOFTWARE: FastSeq for Windows Version 3.0		
		; SEQ ID NO 3950		
		; LENGTH: 380		
		; TYPE: DNA		
		; ORGANISM: Homo sapiens		
		; FEATURE:		
		; NAME/KEY: misc_feature		
		; LOCATION: (1)...(380)		
		; OTHER INFORMATION: n = A,T,C or G		
		US-09-918-995-3950		
		Query Match	99.4%; Score 158; DB 3; Length 380;	
		Best Local Similarity	99.4%; Pred. No. 4.5e-37;	
		Matches 158; Conservative	0; Mismatches 1; Indels 0; Gaps 0;	
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	Db	182	ATGGAGAAAGTCCAATACTCACTCGCTCAGCTATAAGAAGAGGCTCAACCATTTCAAATG	241
	Qy	61	CCTCAACAAGCACGCTCAAAAAGCTACAGAATCTATTATTCATTTCTGTCTCATCTTAATA	120
	Db	242	CCTCAACAAGCACGCTCAAAAAGCTACAGAATCTATTATCAATTTCTGTCTCATCTTAATA	301
	Qy	121	TGTCCTTGCTGATCTGTATCATCTGATGCTTCTCTGA	159
	Db	302	TGTCCTTGCTGATCTGTATCATCTGATGCTTCTCTGA	340
		RESULT 7		
		US-09-918-995-5235		
		; Sequence 5235, Application US/09918995		
		; Publication No. US20030073623A1		
		; GENERAL INFORMATION:		
		; APPLICANT: Hyseq, Inc.		
		; TITLE OF INVENTION: NOVEL NUCLEIC ACID SEQUENCES OBTAINED		
		; FILE REFERENCE: 20411-756		
		; CURRENT APPLICATION NUMBER: US/09/918,995		
		; CURRENT FILING DATE: 2001-07-30		
		; PRIOR APPLICATION NUMBER: US/09/235,076		
		; PRIOR FILING DATE: 1999-01-20		
		; NUMBER OF SEQ ID NOS: 38054		
		; SOFTWARE: FastSeq for Windows Version 3.0		
		; SEQ ID NO 5235		
		; LENGTH: 418		
		; TYPE: DNA		
		Query Match	100.0%; Score 159; DB 10; Length 1712;	
		Best Local Similarity	100.0%; Pred. No. 4.3e-37;	
		Matches 159; Conservative	0; Mismatches 0; Indels 0; Gaps 0;	
	Qy	1	ATGGAGAAAGTCCAATACTCACTCGCTCAGCTATAAGAAGAGGCTCAACCATTTCAAATG	60
	Db	182	ATGGAGAAAGTCCAATACTCACTCGCTCAGCTATAAGAAGAGGCTCAACCATTTCAAATG	241
	Qy	61	CCTCAACAAGCACGCTCAAAAAGCTACAGAATCTATTATTCATTTCTGTCTCATCTTAATA	120
	Db	242	CCTCAACAAGCACGCTCAAAAAGCTACAGAATCTATTATCAATTTCTGTCTCATCTTAATA	301
	Qy	121	TGTCCTTGCTGATCTGTATCATCTGATGCTTCTCTGA	159
	Db	302	TGTCCTTGCTGATCTGTATCATCTGATGCTTCTCTGA	340
		RESULT 5		
		US-11-019-855-1		
		; Sequence 1, Application US/11019855		
		; Publication No. US2005015871A1		
		; GENERAL INFORMATION:		
		; APPLICANT: Hoffmann-La Roche Inc.		
		; TITLE OF INVENTION: novel targets for obesity from skeletal muscle		
		; FILE REFERENCE: case 22314		
		; CURRENT APPLICATION NUMBER: US/11/019,855		
		; CURRENT FILING DATE: 2004-12-22		
		; NUMBER OF SEQ ID NOS: 70		
		; SOFTWARE: PatentIn version 3.2		
		; SEQ ID NO 1		
		; LENGTH: 1712		
		; TYPE: DNA		
		; ORGANISM: Homo sapiens		
		; FEATURE:		
		; NAME/KEY: phospholamban (PLN)		
		; LOCATION: (1)..(1712)		
		; OTHER INFORMATION: accession No.s: NM002667.2; Hs.85050; LocusID: 5350		
		US-11-019-855-1		
		Query Match		


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; TITLE OF INVENTION: FROM VARIOUS CDNA LIBRARIES
; FILE REFERENCE: 20411-756
; CURRENT APPLICATION NUMBER: US/09/918,995
; CURRENT FILING DATE: 2001-07-30
; PRIOR APPLICATION NUMBER: US/09/235,076
; PRIOR FILING DATE: 1999-01-20
; NUMBER OF SEQ ID NOS: 38054
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 5377
; LENGTH: 487
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (1)...(487)
; OTHER INFORMATION: n = A,T,C or G
US-09-918-995-5377

Query Match 93.0%; Score 147.8; DB 3; Length 487;
Best Local Similarity 95.6%; Pred. No. 5.8e-34;
Matches 152; Conservative 0; Mismatches 7; Indels 0; Gaps 0;

QY 1 ATGGAGAAAGTCCATACCTCACTCGCTCAGCTATAGAAGAGCCTCAACCAATTGAAATG 60
DB 252 ATGGAATACGTTCTGTACTCTCACTCGCTCAGCTATAGAAGAGCCTCAACCAATTG 311
QY 61 CCTCAACAAGCAGCTCAAAAGCTACAGAACTATTATCAATTTCTGTCTCATCTTAATA 120
DB 312 CCTCAACAAGCAGCTCAAAAGCTACAGAACTATTATCAATTTCTGTCTCATCTTAATA 371
QY 121 TGTCTTTGCTGATCTGTATCATCTGATGCTTCTCTGA 159
DB 372 TGTCTTTGCTGATCTGTATCATCTGATGCTTCTCTGA 410

RESULT 10
US-09-918-995-17377
; Sequence 17377, Application US/09918995
; Publication No. US20030073623A1
; GENERAL INFORMATION:
; APPLICANT: Hyseq, Inc.
; TITLE OF INVENTION: NOVEL NUCLEIC ACID SEQUENCES OBTAINED
; FILE REFERENCE: 20411-756
; CURRENT APPLICATION NUMBER: US/09/918,995
; CURRENT FILING DATE: 2001-07-30
; PRIOR APPLICATION NUMBER: US/09/235,076
; PRIOR FILING DATE: 1999-01-20
; NUMBER OF SEQ ID NOS: 38054
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 17377
; LENGTH: 492
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (1)...(492)
; OTHER INFORMATION: n = A,T,C or G
US-09-918-995-17377

Query Match 93.0%; Score 147.8; DB 3; Length 492;
Best Local Similarity 95.6%; Pred. No. 5.8e-34;
Matches 152; Conservative 0; Mismatches 7; Indels 0; Gaps 0;

QY 1 ATGGAGAAAGTCCATACCTCACTCGCTCAGCTATAGAAGAGCCTCAACCAATTGAAATG 60
DB 278 ATGGAGAAAGGCCAATACCTCACTCGCTCAGCTATAGAAGAGCCTCAACCAATTGAAATG 337
QY 61 CCTCAACAAGCAGCTCAAAAGCTACAGAACTATTATCAATTTCTGTCTCATCTTAATA 120
DB 338 CCTCAACAAGCAGCTCAAAAGCTACAGAACTATTATCAATTTCTGTCTCATCTTAATA 397
QY 121 TGTCTTTGCTGATCTGTATCATCTGATGCTTCTCTGA 159
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```
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (1)...(418)
; OTHER INFORMATION: n = A,T,C or G
US-09-918-995-5235

Query Match 99.4%; Score 158; DB 3; Length 418;
Best Local Similarity 99.4%; Pred. No. 4.7e-37;
Matches 158; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 ATGGAGAAAGTCCATACCTCACTCGCTCAGCTATAGAAGAGCCTCAACCAATTGAAATG 60
DB 156 ATGGAGAAAGTCCATACCTCACTCGCTCAGCTATAGAAGAGCCTCAACCAATTGAAATG 215
QY 61 CCTCAACAAGCAGCTCAAAAGCTACAGAACTATTATCAATTTCTGTCTCATCTTAATA 120
DB 216 CCTCAACAAGCAGCTCAAAAGCTACAGAACTATTATCAATTTCTGTCTCATCTTAATA 275
QY 121 TGTCTTTGCTGATCTGTATCATCTGATGCTTCTCTGA 159
DB 276 TGTCTTTGCTGATCTGTATCATCTGATGCTTCTCTGA 314

RESULT 8
US-09-918-995-4217
; Sequence 4217, Application US/09918995
; Publication No. US20030073623A1
; GENERAL INFORMATION:
; APPLICANT: Hyseq, Inc.
; TITLE OF INVENTION: NOVEL NUCLEIC ACID SEQUENCES OBTAINED
; FILE REFERENCE: 20411-756
; CURRENT APPLICATION NUMBER: US/09/918,995
; CURRENT FILING DATE: 2001-07-30
; PRIOR APPLICATION NUMBER: US/09/235,076
; PRIOR FILING DATE: 1999-01-20
; NUMBER OF SEQ ID NOS: 38054
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 4217
; LENGTH: 394
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (1)...(394)
; OTHER INFORMATION: n = A,T,C or G
US-09-918-995-4217

Query Match 99.0%; Score 157.4; DB 3; Length 394;
Best Local Similarity 99.4%; Pred. No. 7e-37;
Matches 158; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 ATGGAGAAAGTCCATACCTCACTCGCTCAGCTATAGAAGAGCCTCAACCAATTGAAATG 60
DB 182 ATGGAGAAAGTCCATACCTCACTCGCTCAGCTATAGAAGAGCCTCAACCAATTGAAATG 241
QY 61 CCTCAACAAGCAGCTCAAAAGCTACAGAACTATTATCAATTTCTGTCTCATCTTAATA 120
DB 242 CCTCAACAAGCAGCTCAAAAGCTACAGAACTATTATCAATTTCTGTCTCATCTTAATA 301
QY 121 TGTCTTTGCTGATCTGTATCATCTGATGCTTCTCTGA 159
DB 302 TGTCTTTGCTGATCTGTATCATCTGATGCTTCTCTGA 340

RESULT 9
US-09-918-995-5377
; Sequence 5377, Application US/09918995
; Publication No. US20030073623A1
; GENERAL INFORMATION:
; APPLICANT: Hyseq, Inc.
; TITLE OF INVENTION: NOVEL NUCLEIC ACID SEQUENCES OBTAINED
```

```
Db 398 TGTCCCTTGCTGATCTGTATCATCGTGAAGCTTCTTTGA 436
|||||
Query Match 90.9%; Score 144.6; DB 3; Length 407;
Best Local Similarity 94.3%; Pred. No. 4.9e-33;
Matches 150; Conservative 0; Mismatches 9; Indels 0; Gaps 0;

RESULT 11
US-10-371-101-13
; Sequence 13, Application US/10371101
; Publication No. US20030149995A1
; GENERAL INFORMATION:
; APPLICANT: Zwaal, Richard
; APPLICANT: Groenen, Jose
; APPLICANT: Bogaert, Thierry
; TITLE OF INVENTION: COMPOUND SCREENING METHODS
; FILE REFERENCE: D00590.70035.US
; CURRENT APPLICATION NUMBER: US/10/371,101
; CURRENT FILING DATE: 2003-02-21
; PRIOR FILING DATE: 1999-04-15
; PRIOR APPLICATION NUMBER: US 60/129,596
; PRIOR FILING DATE: 1999-06-01
; PRIOR APPLICATION NUMBER: 09/549,872
; PRIOR FILING DATE: 2000-04-14
; NUMBER OF SEQ ID NOS: 39
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 13
; LENGTH: 159
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: HUMANIZED PIG
; OTHER INFORMATION: PLB cdNA
US-10-371-101-13

Query Match 90.9%; Score 144.6; DB 6; Length 159;
Best Local Similarity 94.3%; Pred. No. 3.3e-33;
Matches 150; Conservative 0; Mismatches 9; Indels 0; Gaps 0;

Qy 1 ATGGAGAAAGTCCAAATACCTCACTCGCTACAGTATAGAAGAGCCTCAACCATTTGAAATG 60
|||||
Db 1 ATGGAGAAAGTCCAAATACCTCACTCGCTACAGTATAGAAGAGCCTCAACCATTTGAAATG 60
|||||

Qy 61 CCTCAACAGCAGCTCAAAAGCTACAGATCTATTATCAATTTCTGCTCATCTTAATA 120
|||||
Db 61 CCTCAACAGCAGCTCAAAAGCTACAGATCTATTATCAATTTCTGCTCATCTTAATA 120
|||||

Qy 121 TGTCTCTTGCTGATCTGTATCATCGTATCTCTCTGA 159
|||||
Db 121 TGCCTCTTGCTGATTTGCATCATCGTATCTCTCTGA 159
|||||

RESULT 12
US-09-918-995-3842
; Sequence 3842, Application US/09918995
; Publication No. US20030073623A1
; GENERAL INFORMATION:
; APPLICANT: Hyseq, Inc.
; TITLE OF INVENTION: NOVEL NUCLEIC ACID SEQUENCES OBTAINED
; FILE REFERENCE: 20411-756
; CURRENT APPLICATION NUMBER: US/09/918,995
; CURRENT FILING DATE: 2001-07-30
; PRIOR APPLICATION NUMBER: US/09/235,076
; PRIOR FILING DATE: 1999-01-20
; NUMBER OF SEQ ID NOS: 38054
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 3842
; LENGTH: 407
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-918-995-3842

Db 398 TGTCCCTTGCTGATCTGTATCATCGTGAAGCTTCTTTGA 436
|||||
Query Match 90.9%; Score 144.6; DB 3; Length 407;
Best Local Similarity 94.3%; Pred. No. 4.9e-33;
Matches 150; Conservative 0; Mismatches 9; Indels 0; Gaps 0;

RESULT 13
US-10-371-101-9
; Sequence 9, Application US/10371101
; Publication No. US20030149995A1
; GENERAL INFORMATION:
; APPLICANT: Zwaal, Richard
; APPLICANT: Groenen, Jose
; APPLICANT: Bogaert, Thierry
; TITLE OF INVENTION: COMPOUND SCREENING METHODS
; FILE REFERENCE: D00590.70035.US
; CURRENT APPLICATION NUMBER: US/10/371,101
; CURRENT FILING DATE: 2003-02-21
; PRIOR FILING DATE: 1999-04-15
; PRIOR APPLICATION NUMBER: GB 9908670.4
; PRIOR FILING DATE: 1999-04-15
; PRIOR APPLICATION NUMBER: US 60/129,596
; PRIOR FILING DATE: 1999-04-15
; PRIOR APPLICATION NUMBER: GB 9912736.7
; PRIOR FILING DATE: 1999-06-01
; PRIOR APPLICATION NUMBER: 09/549,872
; PRIOR FILING DATE: 2000-04-14
; NUMBER OF SEQ ID NOS: 39
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 9
; LENGTH: 159
; TYPE: DNA
; ORGANISM: Sus sp.
US-10-371-101-9

Query Match 89.9%; Score 143; DB 6; Length 159;
Best Local Similarity 93.7%; Pred. No. 9.9e-33;
Matches 149; Conservative 0; Mismatches 10; Indels 0; Gaps 0;

Qy 1 ATGGAGAAAGTCCAAATACCTCACTCGCTACAGTATAGAAGAGCCTCAACCATTTGAAATG 60
|||||
Db 1 ATGGAGAAAGTCCAAATACCTCACTCGCTACAGTATAGAAGAGCCTCAACCATTTGAAATG 60
|||||

Qy 61 CCTCAACAGCAGCTCAAAAGCTACAGATCTATTATCAATTTCTGCTCATCTTAATA 120
|||||
Db 61 CCTCAACAGCAGCTCAAAAGCTACAGATCTATTATCAATTTCTGCTCATCTTAATA 120
|||||

Qy 121 TGTCTCTTGCTGATCTGTATCATCGTATCTCTCTGA 159
|||||
Db 121 TGCCTCTTGCTGATTTGCATCATCGTATCTCTCTGA 159
|||||

RESULT 14
US-10-815-514-26
; Sequence 26, Application US/10815514
; Publication No. US20040204361A1
; GENERAL INFORMATION:
; APPLICANT: Rothman, James
; APPLICANT: Mayhew, Mark
; APPLICANT: Hoe, Mee
; TITLE OF INVENTION: KDEL RECEPTOR INHIBITORS
; FILE REFERENCE: 31488
; CURRENT APPLICATION NUMBER: US/10/815,514
```

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; CURRENT FILING DATE: 2004-03-31
; PRIOR APPLICATION NUMBER: US/09/696,872
; PRIOR FILING DATE: 2000-10-26
; NUMBER OF SEQ ID NOS: 42
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 26
; LENGTH: 315
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: chimeric human PLB-KDEL
US-10-815-514-26

Query Match      52.2%; Score 83; DB 8; Length 315;
Best Local Similarity 100.0%; Pred. No. 1.3e-14; Indels 0; Gaps 0;
Matches 83; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 74 GTCAAAGCTACAGAACTCTATTATCAATTTCTGCTCATCTTAATATGCTCTTGCTGA 133
Db 98 GTCAAAGCTACAGAACTCTATTATCAATTTCTGCTCATCTTAATATGCTCTTGCTGA 157

QY 134 TCTGTATCATCGTGATGCTTCTC 156
Db 158 TCTGTATCATCGTGATGCTTCTC 180

RESULT 15
US-10-877-930-26
; Sequence 26, Application US/10877930
; Publication No. US20040235129A1
; GENERAL INFORMATION:
; APPLICANT: Rothman, James
; APPLICANT: Mayhew, Mark
; APPLICANT: Hoe, Mee
; TITLE OF INVENTION: KDEL RECEPTOR INHIBITORS
; FILE REFERENCE: 31488
; CURRENT APPLICATION NUMBER: US/10/877,930
; CURRENT FILING DATE: 2004-06-25
; PRIOR APPLICATION NUMBER: US/09/696,070
; PRIOR FILING DATE: 2000-10-25
; NUMBER OF SEQ ID NOS: 42
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 26
; LENGTH: 315
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: chimeric human PLB-KDEL
US-10-877-930-26

Query Match      52.2%; Score 83; DB 8; Length 315;
Best Local Similarity 100.0%; Pred. No. 1.3e-14; Indels 0; Gaps 0;
Matches 83; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 74 GTCAAAGCTACAGAACTCTATTATCAATTTCTGCTCATCTTAATATGCTCTTGCTGA 133
Db 98 GTCAAAGCTACAGAACTCTATTATCAATTTCTGCTCATCTTAATATGCTCTTGCTGA 157

QY 134 TCTGTATCATCGTGATGCTTCTC 156
Db 158 TCTGTATCATCGTGATGCTTCTC 180

RESULT 16
US-10-873-594-26
; Sequence 26, Application US/10873594
; Publication No. US20050095667A1
; GENERAL INFORMATION:
; APPLICANT: Rothman, James
; APPLICANT: Mayhew, Mark
; APPLICANT: Hoe, Mee
; TITLE OF INVENTION: KDEL RECEPTOR INHIBITORS
; FILE REFERENCE: A31488-I-I 065360.0152
US-10-873-594-26

Query Match      52.2%; Score 83; DB 9; Length 315;
Best Local Similarity 100.0%; Pred. No. 1.3e-14; Indels 0; Gaps 0;
Matches 83; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 74 GTCAAAGCTACAGAACTCTATTATCAATTTCTGCTCATCTTAATATGCTCTTGCTGA 133
Db 98 GTCAAAGCTACAGAACTCTATTATCAATTTCTGCTCATCTTAATATGCTCTTGCTGA 157

QY 134 TCTGTATCATCGTGATGCTTCTC 156
Db 158 TCTGTATCATCGTGATGCTTCTC 180

RESULT 17
US-10-724-532-3
; Sequence 3, Application US/10724532
; Publication No. US20040203027A1
; GENERAL INFORMATION:
; APPLICANT: Reed, Thomas D
; TITLE OF INVENTION: Signal for Targeting Molecules to the Sarco(endo)plasmic
; FILE REFERENCE: Reticulum
; CURRENT APPLICATION NUMBER: US/10/724,532
; CURRENT FILING DATE: 2003-11-29
; PRIOR APPLICATION NUMBER: US 60/430322
; PRIOR FILING DATE: 2002-12-02
; NUMBER OF SEQ ID NOS: 6
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 3
; LENGTH: 108
; TYPE: DNA
; ORGANISM: mus musculus
US-10-724-532-3

Query Match      28.9%; Score 46; DB 8; Length 108;
Best Local Similarity 65.7%; Pred. No. 0.001;
Matches 67; Conservative 0; Mismatches 35; Indels 0; Gaps 0;

QY 54 TGAATGCTCTCAACAGCAGCGTCAAAAGCTACAGAACTCTTAATATGCTCTTGCTCAT 113
Db 6 TGAGAGAGGCGCTCAGGCCAGGAGAACTCCAGAAATGCTTTTCAATGCTTTTGTCTGAT 65

QY 114 CTTAATATGCTCTTGTGCTGATCTGTATCATCGTGATGCTTCT 155
Db 66 TCTCATCTGCTCTGCTGATTTTGCATTATCGTATGCTCTCT 107

RESULT 18
US-10-724-532-4/c
; Sequence 4, Application US/10724532
; Publication No. US20040203027A1
; GENERAL INFORMATION:
; APPLICANT: Reed, Thomas D
; TITLE OF INVENTION: Signal for Targeting Molecules to the Sarco(endo)plasmic
; FILE REFERENCE: Reticulum
```

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; FILE REFERENCE: SR RPA
; CURRENT APPLICATION NUMBER: US/10/724,532
; CURRENT FILING DATE: 2003-11-29
; PRIOR APPLICATION NUMBER: US 60/430322
; PRIOR FILING DATE: 2002-12-02
; NUMBER OF SEQ ID NOS: 6
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 4
; LENGTH: 108
; TYPE: DNA
; ORGANISM: mus musculus
US-10-724-532-4

Query Match      28.9%; Score 46; DB 8; Length 108;
Best Local Similarity 65.7%; Pred. No. 0.001;
Matches 67; Conservative 0; Mismatches 35; Indels 0; Gaps 0;

QY 54 TGAATGCTCTCAACAGCAGCTCAAAAGCTACAGAACTCTATTATCAATTTCTGTCTCAT 113
DB 103 TGAGAGAGGCTCTAGGCGAGCAACCTCCAGAACTGTTTCATTGCTTTTGTCTCAT 44
QY 114 CTTAATATGCTCTTGTGCTGATCTGATCATCTGATGCTTCT 155
DB 43 TCTCATCTGCTCTGCTGCTGATTTGCAATTAATGTCATGCTCT 2

RESULT 19
US-10-724-532-5
; Sequence 5, Application US/10724532
; Publication No. US20040203027A1
; GENERAL INFORMATION:
; APPLICANT: Reed, Thomas D
; TITLE OF INVENTION: Signal for Targeting Molecules to the Sarco(endo)plasmic
; FILE REFERENCE: SR RPA
; CURRENT APPLICATION NUMBER: US/10/724,532
; CURRENT FILING DATE: 2003-11-29
; PRIOR APPLICATION NUMBER: US 60/430322
; PRIOR FILING DATE: 2002-12-02
; NUMBER OF SEQ ID NOS: 6
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 5
; LENGTH: 135
; TYPE: DNA
; ORGANISM: mus musculus
US-10-724-532-5

Query Match      28.9%; Score 46; DB 8; Length 135;
Best Local Similarity 65.7%; Pred. No. 0.001;
Matches 67; Conservative 0; Mismatches 35; Indels 0; Gaps 0;

QY 54 TGAATGCTCTCAACAGCAGCTCAAAAGCTACAGAACTCTATTATCAATTTCTGTCTCAT 113
DB 18 TGAGAGAGGCTCTAGGCGAGCAACCTCCAGAACTGCTTTTCATTGCTTTTGTCTCAT 77
QY 114 CTTAATATGCTCTTGTGCTGATCTGATCATCTGATGCTTCT 155
DB 78 TCTCATCTGCTCTGCTGCTGATTTGCAATTAATGTCATGCTCTCT 119

RESULT 20
US-10-724-532-6/c
; Sequence 6, Application US/10724532
; Publication No. US20040203027A1
; GENERAL INFORMATION:
; APPLICANT: Reed, Thomas D
; TITLE OF INVENTION: Signal for Targeting Molecules to the Sarco(endo)plasmic
; FILE REFERENCE: SR RPA
; CURRENT APPLICATION NUMBER: US/10/724,532
; CURRENT FILING DATE: 2003-11-29
; PRIOR APPLICATION NUMBER: US 60/430322
; PRIOR FILING DATE: 2002-12-02
```

```
; NUMBER OF SEQ ID NOS: 6
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 6
; LENGTH: 135
; TYPE: DNA
; ORGANISM: mus musculus
US-10-724-532-6
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```
Query Match      28.9%; Score 46; DB 8; Length 135;
Best Local Similarity 65.7%; Pred. No. 0.001;
Matches 67; Conservative 0; Mismatches 35; Indels 0; Gaps 0;
```

```
QY 54 TGAATGCTCTCAACAGCAGCTCAAAAGCTACAGAACTCTATTATCAATTTCTGTCTCAT 113
DB 118 TGAGAGAGGCTCTAGGCGAGCAACCTCCAGAACTGCTTTTCATTGCTTTTGTCTCAT 59
QY 114 CTTAATATGCTCTTGTGCTGATCTGATCATCTGATGCTTCT 155
DB 58 TCTCATCTGCTCTGCTGCTGATTTGCAATTAATGTCATGCTCT 17
```

```
RESULT 21
US-09-925-065A-575150/c
; Sequence 575150, Application US/09925065A
; Publication No. US20050228172A9
; GENERAL INFORMATION:
; APPLICANT: Wang, David G.
; TITLE OF INVENTION: Identification and Mapping of Single
; FILE REFERENCE: 108827.135
; CURRENT APPLICATION NUMBER: US/09/925,065A
; CURRENT FILING DATE: 2001-08-08
; PRIOR APPLICATION NUMBER: US 60/243,096
; PRIOR FILING DATE: 2000-10-24
; PRIOR FILING DATE: 2000-11-20
; PRIOR APPLICATION NUMBER: US 60/252,147
; PRIOR FILING DATE: 2000-11-20
; PRIOR APPLICATION NUMBER: US 60/250,092
; PRIOR FILING DATE: 2000-11-30
; PRIOR APPLICATION NUMBER: US 60/261,766
; PRIOR FILING DATE: 2001-01-16
; PRIOR APPLICATION NUMBER: US 60/289,846
; NUMBER OF SEQ ID NOS: 957086
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 575150
; LENGTH: 589
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-925-065A-575150
```

```
Query Match      21.5%; Score 34.2; DB 4; Length 589;
Best Local Similarity 52.4%; Pred. No. 7;
Matches 75; Conservative 0; Mismatches 68; Indels 0; Gaps 0;
```

```
QY 1 ATGGAGAAAGTCCAATACCTCACTCGCTCAGCTATAAGAGAGCCTCAACCAATTGAAATG 60
DB 284 AAGGAAAAGACTAATAATACATTGAACCTCCWATATTTTGGAACTACTGTTTAAACATTGAACAA 225
QY 61 CCTCAACAAGCAGCTCAAAAGCTACAGAACTCTATTATCAATTTCTGTCTCATTTAATA 120
DB 224 CAACAACAAAATCCCCAAATATACATACCTTCCTCCATTATAGAAAATTTAAAG 165
QY 121 TGTCTCTTGTGCTGATCTGATCAT 143
DB 164 TAATCAAAACTAATCCATAGAT 142
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```
RESULT 22
US-09-925-065A-575151/c
; Sequence 575151, Application US/09925065A
; Publication No. US20050228172A9
; GENERAL INFORMATION:
; APPLICANT: Wang, David G.
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; TITLE OF INVENTION: Identification and Mapping of Single
; FILE REFERENCE: 108827.135
; CURRENT APPLICATION NUMBER: US/09/925,065A
; CURRENT FILING DATE: 2001-08-08
; PRIOR APPLICATION NUMBER: US 60/243,096
; PRIOR FILING DATE: 2000-10-24
; PRIOR APPLICATION NUMBER: US 60/252,147
; PRIOR FILING DATE: 2000-11-20
; PRIOR APPLICATION NUMBER: US 60/250,092
; PRIOR FILING DATE: 2000-11-30
; PRIOR APPLICATION NUMBER: US 60/261,766
; PRIOR FILING DATE: 2001-01-16
; PRIOR APPLICATION NUMBER: US 60/289,846
; PRIOR FILING DATE: 2001-05-09
; NUMBER OF SEQ ID NOS: 957086
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 575151
; LENGTH: 589
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-925-065A-575151
Query Match 21.5%; Score 34.2; DB 4; Length 589;
Best Local Similarity 52.4%; Pred. No. 7;
Matches 75; Conservative 0; Mismatches 68; Indels 0; Gaps 0;
QY 1 ATGGAGAAAGTCCAACTACTCTCCTCAGCTATAGAGAGCCCTCAACCAATTGAATG 60
DB 284 AAGGAAAAAGACTAATACATGAATGCAATATTTTGGAACTACTGTTAACATTTGAACAA 225
QY 61 CCTCAACAAGCAGCTCAAAAGCTACAGATCTATTTATCAATTTCTGCTCATCTTAATA 120
DB 224 CAACAACAAAATCCCAATATACATCTTCACTCTTCCATTTATAGAAAATTTAAAG 165
QY 121 TGTCTCTTGTGATCTGTATCAT 143
DB 164 TAATCAAACTAATCCATAGAT 142
RESULT 23
US-10-719-993-6822/c
; Sequence 6822, Application US/10719993
; Publication No. US20040265849A1
; GENERAL INFORMATION:
; APPLICANT: CARGILL, Michele et al.
; TITLE OF INVENTION: GENETIC POLYMORPHISMS ASSOCIATED WITH
; FILE REFERENCE: CL001496
; CURRENT APPLICATION NUMBER: US/10/719,993
; CURRENT FILING DATE: 2003-11-24
; NUMBER OF SEQ ID NOS: 55342
; SOFTWARE: Fast-SEQ for Windows Version 4.0
; SEQ ID NO 6822
; LENGTH: 786452
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (1)_(786452)
; OTHER INFORMATION: n = A,T,C or G, or insertion/deletion polymorphism (see Tables 1-
US-10-719-993-6822
Query Match 21.5%; Score 34.2; DB 8; Length 786452;
Best Local Similarity 52.4%; Pred. No. 1.4e+02;
Matches 75; Conservative 0; Mismatches 68; Indels 0; Gaps 0;
QY 1 ATGGAGAAAGTCCAACTACTCTCAGCTATAGAGAGCCCTCAACCAATTGAATG 60
DB 640845 AAGGAAAAAGACTAATACATTTGAATCTCCWATATTTTGGAACTACTGTTAACATTTGAACAA 640786
QY 61 CCTCAACAAGCAGCTCAAAAGCTACAGATCTATTTATCAATTTCTGTCTCATCTTAATA 120

Db 640785 CAACAACAAAATCCCAATATACATCTTCACTCTTCCATTTATAGAAAATTTAAAG 640726
QY 121 TGTCTCTTGTGATCTGTATCAT 143
DB 640725 TAATCAAAACTAATCCATAGAT 640703
RESULT 24
US-10-311-455-2169/c
; Sequence 2169, Application US/10311455
; Publication No. US20030143606A1
; GENERAL INFORMATION:
; APPLICANT: OLEK, Alexander
; APPLICANT: PIEPENBROCK, Christian
; APPLICANT: BERLIN, Kurt
; TITLE OF INVENTION: Diagnosis of Diseases Associated with the Immune System by Determin
; FILE REFERENCE: 5013.1014
; CURRENT APPLICATION NUMBER: US/10/311,455
; CURRENT FILING DATE: 2002-12-16
; PRIOR APPLICATION NUMBER: PCT/EP01/07537
; PRIOR FILING DATE: 2001-07-02
; PRIOR APPLICATION NUMBER: DE 10032529.7
; PRIOR FILING DATE: 2000-06-30
; PRIOR APPLICATION NUMBER: DE 10043826.1
; PRIOR FILING DATE: 2000-09-01
; NUMBER OF SEQ ID NOS: 2424
; SEQ ID NO 2169
; LENGTH: 37973
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: chemically treated genomic DNA (Homo sapiens)
US-10-311-455-2169
Query Match 21.0%; Score 33.4; DB 6; Length 37973;
Best Local Similarity 62.7%; Pred. No. 68;
Matches 52; Conservative 0; Mismatches 31; Indels 0; Gaps 0;
QY 72 ACGTCAAAAGCTACAGAATCTATTTATCAATTTCTGTCTCATCTTAATATGCTCTTGCT 131
DB 12130 ACTTCACATTTATAAATATATTTATCTATAATTTCTTTCTTATAATATCTTTTCTCT 12071
QY 132 GATCTGATCATCGTGATGCTTC 154
DB 13070 AATTTTAAACAACAAATAATAC 12048
RESULT 25
US-10-719-993-26457/c
; Sequence 26457, Application US/10719993
; Publication No. US20040265849A1
; GENERAL INFORMATION:
; APPLICANT: CARGILL, Michele et al.
; TITLE OF INVENTION: GENETIC POLYMORPHISMS ASSOCIATED WITH
; FILE REFERENCE: CL001496
; CURRENT APPLICATION NUMBER: US/10/719,993
; CURRENT FILING DATE: 2003-11-24
; NUMBER OF SEQ ID NOS: 55342
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 26457
; LENGTH: 201
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-719-993-26457
Query Match 20.9%; Score 33.2; DB 8; Length 201;
Best Local Similarity 55.1%; Pred. No. 8.9;
Matches 65; Conservative 0; Mismatches 53; Indels 0; Gaps 0;
QY 1 ATGGAGAAAGTCCAACTACTCTCGCTCAGCTATAAGAGAGCCCTCAACCAATTGAATG 60

Db 129 AAGGAAAGACTAATACTGAACCTCCWATATTTTGGAACTCTTTAAACATTTGAACAA 70
Qy 61 CCTCAACAGCAGCTCAAGAGCTACAGAACTCTATTTATCAATTTCTGCTCATCTTAA 118
Db 69 CAACAACAAATCCCAATATACATCTTCACTCTTCCATTTATAGAAATTTAA 12

RESULT 26
US-10-388-838-1/c
; Sequence 1, Application US/10388838
; Publication No. US20040180344A1
; GENERAL INFORMATION:
; APPLICANT: David W. Morris
; APPLICANT: Marc Malandro
; TITLE OF INVENTION: Novel Therapeutic Targets in Cancer
; FILE REFERENCE: 529452001600
; CURRENT APPLICATION NUMBER: US/10/388,838
; CURRENT FILING DATE: 2003-03-14
; NUMBER OF SEQ ID NOS: 114
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 1
; LENGTH: 170279
; TYPE: DNA
; ORGANISM: Mus musculus
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (1)..(170279)
; OTHER INFORMATION: n = A,T,C or G
US-10-388-838-1

Query Match 20.5%; Score 32.6; DB 8; Length 170279;
Best Local Similarity 51.7%; Pred. No. 2.2e+02;
Matches 74; Conservative 0; Mismatches 69; Indels 0; Gaps 0;

Qy 15 ATACCTCAGCTCGCTCAGCTATAGAGAGGCTCAACCAATTTGAATGCTCTTAATATGCTCTTCTGCTGAT 74
Db 142522 AAGCTCAGATCTTTTGTATGATATAGCTCAGTTCCTTGGCAATGACTAACTGATCACA 142463

Qy 75 TCAAAAGCTACAGAACTATTTATCAATTTCTGCTCATCTTAATATGCTCTTCTGCTGAT 134
Db 142462 GAATAAGCTGAGTATATATGCAACTTAAATTTGTTTCATGCTGTTTCACTGCTCCCT 142403

Qy 135 CTGTATCATGCTGATGCTTCTCT 157
Db 142402 TTATTTCTTATGTTTGGACCTCT 142380

RESULT 27
US-11-029-984-845/c
; Sequence 845, Application US/11029984
; Publication No. US20050196784A1
; GENERAL INFORMATION:
; APPLICANT: Reymondottir, Inga
; APPLICANT: Gulcher, Jeffrey R.
; APPLICANT: Grant, Struan F.
; APPLICANT: Thorleifsson, Gudmar
; TITLE OF INVENTION: Human Type II Diabetes Gene-Kv Channel-Interacting Protein (KCHIP)
; TITLE OF INVENTION: Located on Chromosome 5
; FILE REFERENCE: 2345, 2049-007
; CURRENT APPLICATION NUMBER: US/11/029,984
; CURRENT FILING DATE: 2005-01-05
; NUMBER OF SEQ ID NOS: 979
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 845
; LENGTH: 402
; TYPE: DNA
; ORGANISM: Homo sapiens
US-11-029-984-845

Query Match 20.3%; Score 32.2; DB 10; Length 402;
Best Local Similarity 56.0%; Pred. No. 24;
Matches 61; Conservative 0; Mismatches 48; Indels 0; Gaps 0;

Qy 51 CATTGAAATGCTCAACAGCAGCTCAAAAGCTACAGAACTCTATTTATCAATTTCTGCT 110
Db 251 CCTAGAGTCAAGAAAGCAAGGGTTATAAACAGAAATATCTATCAGTGTACCCAT 192

Qy 111 CATCTTAATATGCTCTTCTGCTGATCTGATCATCTGATGCTGCTCTCTCA 159
Db 191 CTTCTCTGTGCTCAATCTGCTCTCACTTTGTCTATATCATCTCTCTCTTA 143

RESULT 28
US-09-925-065A-150093
; Sequence 150093, Application US/09925065A
; Publication No. US20050228172A9
; GENERAL INFORMATION:
; APPLICANT: Wang, David G.
; TITLE OF INVENTION: Identification and Mapping of Single
; FILE REFERENCE: 108827.135
; CURRENT APPLICATION NUMBER: US/09/925,065A
; CURRENT FILING DATE: 2001-08-08
; PRIOR APPLICATION NUMBER: US 60/243,096
; PRIOR FILING DATE: 2000-10-24
; PRIOR APPLICATION NUMBER: US 60/252,147
; PRIOR FILING DATE: 2000-11-20
; PRIOR APPLICATION NUMBER: US 60/250,092
; PRIOR FILING DATE: 2000-11-30
; PRIOR APPLICATION NUMBER: US 60/261,766
; PRIOR FILING DATE: 2001-01-16
; PRIOR APPLICATION NUMBER: US 60/289,846
; PRIOR FILING DATE: 2001-05-09
; NUMBER OF SEQ ID NOS: 957086
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 150093
; LENGTH: 451
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-925-065A-150093

Query Match 20.1%; Score 32; DB 4; Length 451;
Best Local Similarity 55.4%; Pred. No. 29;
Matches 62; Conservative 0; Mismatches 50; Indels 0; Gaps 0;

Qy 15 ATACCTCAGCTCGCTCAGCTATAGAGAGGCTCAACCAATTTGAATGCTCTCAACAGCAG 74
Db 213 ATAGCACAGTCTCTTTCTTAAACAGGTCACCCACAAAGTTGTCTCAGCCTAGAGCACT 272

Qy 75 TCAAAAGCTACAGAACTCTATTTATCAATTTCTGCTCATCTTAATATGCTCTC 126
Db 273 TGTAGCAAAAGAAAGTTATTTATACATTTTTTTCTCATCTATAGCTTTCTC 324

RESULT 29
US-10-027-632-140279
; Sequence 140279, Application US/10027632
; Publication No. US20020198371A1
; GENERAL INFORMATION:
; APPLICANT: Wang, David G.
; TITLE OF INVENTION: Identification and Mapping of Single Nucleotide
; FILE REFERENCE: 108827.129
; CURRENT APPLICATION NUMBER: US/10/027,632
; CURRENT FILING DATE: 2002-04-30
; PRIOR APPLICATION NUMBER: US 60/218,006
; PRIOR FILING DATE: 2000-07-12
; PRIOR APPLICATION NUMBER: US 60/198,676
; PRIOR FILING DATE: 2000-04-20
; PRIOR APPLICATION NUMBER: US 60/193,483
; PRIOR FILING DATE: 2000-03-29
; PRIOR APPLICATION NUMBER: US 60/185,218
; PRIOR FILING DATE: 2000-02-24
; PRIOR APPLICATION NUMBER: US 60/167,363
; PRIOR FILING DATE: 1999-11-23
; PRIOR APPLICATION NUMBER: US 60/156,358

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; PRIORITY FILING DATE: 1999-09-28
; PRIORITY APPLICATION NUMBER: US 60/146,002
; PRIORITY FILING DATE: 1999-08-09
; NUMBER OF SEQ ID NOS: 325720
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 140279
; LENGTH: 359
; TYPE: DNA
; ORGANISM: Human
US-10-027-632-140279

Query Match      20.0%; Score 31.8; DB 5; Length 359;
Best Local Similarity 54.8%; Pred. No. 30;
Matches 63; Conservative 0; Mismatches 52; Indels 0; Gaps 0;

QY 34 ATAAGAAGAGCCTCAACCAATGAAATGCCTCAACAGCAGCGTCAAAAGCTACAGAACTCA 93
Db 32 ATCAAAACAGCATTAAACAAGTAACAGGTTTTCAAAGCTTTCTACATGCAAACTTACACA 91

QY 94 TTTATCAATTTCTGCTCATCTTAATATGCTCTTCTGCTGATCTGATCATCGTGA 148
Db 92 ATTATCCCTTTAAATTTTATCTTCTATATATATATATGATGATCTATTTGTTCTGA 146

RESULT 30
US-10-027-632-140279
; Sequence 140279, Application US/10027632
; Publication No. US20030204075A9
; GENERAL INFORMATION:
; APPLICANT: Wang, David G.
; TITLE OF INVENTION: Identification and Mapping of Single Nucleotide
; FILE REFERENCE: 108827.129
; CURRENT APPLICATION NUMBER: US/10/027,632
; CURRENT FILING DATE: 2002-04-30
; PRIORITY FILING DATE: 2000-07-12
; PRIORITY APPLICATION NUMBER: US 60/218,006
; PRIORITY FILING DATE: 2000-04-20
; PRIORITY APPLICATION NUMBER: US 60/198,676
; PRIORITY FILING DATE: 2000-03-29
; PRIORITY APPLICATION NUMBER: US 60/193,483
; PRIORITY FILING DATE: 2000-02-24
; PRIORITY APPLICATION NUMBER: US 60/185,218
; PRIORITY FILING DATE: 1999-11-23
; PRIORITY APPLICATION NUMBER: US 60/167,363
; PRIORITY FILING DATE: 1999-09-28
; PRIORITY APPLICATION NUMBER: US 60/156,358
; PRIORITY FILING DATE: 1999-08-09
; PRIORITY APPLICATION NUMBER: US 60/146,002
; NUMBER OF SEQ ID NOS: 325720
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 140279
; LENGTH: 359
; TYPE: DNA
; ORGANISM: Human
US-10-027-632-140279

Query Match      20.0%; Score 31.8; DB 6; Length 359;
Best Local Similarity 54.8%; Pred. No. 30;
Matches 63; Conservative 0; Mismatches 52; Indels 0; Gaps 0;

QY 34 ATAAGAAGAGCCTCAACCAATGAAATGCCTCAACAGCAGCGTCAAAAGCTACAGAACTCA 93
Db 32 ATCAAAACAGCATTAAACAAGTAACAGGTTTTCAAAGCTTTCTACATGCAAACTTACACA 91

QY 94 TTTATCAATTTCTGCTCATCTTAATATGCTCTTCTGCTGATCTGATCATCGTGA 148
Db 92 ATTATCCCTTTAAATTTTATCTTCTATATATATATGATGATCTATTTGTTCTGA 146

RESULT 31
US-09-925-065A-536994/c
; Sequence 536994, Application US/09925065A
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; Publication No. US20050228172A9
; GENERAL INFORMATION:
; APPLICANT: Wang, David G.
; TITLE OF INVENTION: Identification and Mapping of Single
; FILE REFERENCE: 108827.135
; CURRENT APPLICATION NUMBER: US/09/925,065A
; CURRENT FILING DATE: 2001-08-08
; PRIORITY APPLICATION NUMBER: US 60/243,096
; PRIORITY FILING DATE: 2000-10-24
; PRIORITY APPLICATION NUMBER: US 60/252,147
; PRIORITY FILING DATE: 2000-11-20
; PRIORITY APPLICATION NUMBER: US 60/250,092
; PRIORITY FILING DATE: 2000-11-30
; PRIORITY APPLICATION NUMBER: US 60/261,766
; PRIORITY FILING DATE: 2001-01-16
; PRIORITY APPLICATION NUMBER: US 60/289,846
; PRIORITY FILING DATE: 2001-05-09
; NUMBER OF SEQ ID NOS: 957086
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 536994
; LENGTH: 636
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-925-065A-536994

Query Match      20.0%; Score 31.8; DB 4; Length 636;
Best Local Similarity 59.3%; Pred. No. 38;
Matches 54; Conservative 0; Mismatches 37; Indels 0; Gaps 0;

QY 54 TGAATGCTCAACAGCAGCGTCAAAAGCTACAGAACTTATATCAATTTCTGCTCAT 113
Db 461 TTATAAGATTTTCACATTTAAAGTGAGATGATACAGCATATGCTTTCTGCTGCTTAT 402

QY 114 CTTAATATGCTCTTCTGCTGATCTGTATCATC 144
Db 401 TTCACCTAGTATAATGTTGAACGGTTTCATC 371

RESULT 32
US-08-781-986A-283
; Sequence 283, Application US/08781986A
; Publication No. US20030054436A1
; GENERAL INFORMATION:
; APPLICANT: Charles Kunsch
; TITLE OF INVENTION: Staphylococcus aureus Polynucleotides and Sequences
; NUMBER OF SEQUENCES: 5255
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Human Genome Sciences, Inc.
; STREET: 9410 Key West Avenue
; CITY: Rockville
; STATE: Maryland
; COUNTRY: USA
; ZIP: 20850
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette, 3.50 inch, 1.4Mb storage
; COMPUTER: HP Vectra 486/33
; OPERATING SYSTEM: MSDOS version 6.2
; SOFTWARE: ASCII Text
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/781,986A
; FILING DATE:
; CLASSIFICATION: 435
; PRIORITY APPLICATION DATA:
; APPLICATION NUMBER:
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Benson, Bob
; REGISTRATION NUMBER: 30,446
; REFERENCE/DOCKET NUMBER: PB248PP
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (301) 309-8504
; TELEFAX: (301) 309-8512
```



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; INFORMATION FOR SEQ ID NO: 283:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1421 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: linear
US-08-781-986A-283

Query Match      20.0%; Score 31.8; DB 2; Length 1421;
Best Local Similarity 61.4%; Pred. No. 53;
Matches 51; Conservative 0; Mismatches 32; Indels 0; Gaps 0;

QY 36 AAGAGAGCCTCAACCATTTGAATTCCTCAACAGCAGCTCAAAAGCTACAGAATCTATT 95
Db 317 ACGAAGAAACTGAAATTTGAAATCGGTGGATATCATGTCAAATATATAGTCAAGATGTA 376
QY 96 TATCAATTTCTGTCTCATCTTAA 118
Db 377 CTTCAATTACTCTATATAAATAA 399

RESULT 33
US-10-329-624-283
; Sequence 283, Application US/10329624
; Publication No. US20040043037A1
; GENERAL INFORMATION:
; APPLICANT: Charles Kunsch
; Gil H. Choi
; Patrick S. Dillon
; Craig A. Rosen
; Steven C. Barash
; Michael R. Fannon
; TITLE OF INVENTION: Staphylococcus aureus Polynucleotides and Sequences
; NUMBER OF SEQUENCES: 5256
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Human Genome Sciences, Inc.
; STREET: 9410 Key West Avenue
; CITY: Rockville
; STATE: Maryland
; COUNTRY: USA
; ZIP: 20850
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette, 3.50 inch, 1.4Mb storage
; COMPUTER: HP Vectra 486/33
; OPERATING SYSTEM: MSDOS version 6.2
; SOFTWARE: ASCII Text
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/10/329,624
; FILING DATE: 27-Dec-2002
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/956,171
; FILING DATE: October 20, 1997
; APPLICATION NUMBER: 60/009,861
; FILING DATE: January 5, 1996
; APPLICATION NUMBER: 08/781,986
; FILING DATE: January 3, 1997
; ATTORNEY/AGENT INFORMATION:
; NAME: Mark J. Hyman
; REGISTRATION NUMBER: 46,789
; REFERENCE/DOCKET NUMBER: PB248P1D1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (240) 314-1224
; TELEFAX: (301) 309-8439
; INFORMATION FOR SEQ ID NO: 283:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1421 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: linear
; SEQUENCE DESCRIPTION: SEQ ID NO: 283:
US-10-329-624-283

Query Match      20.0%; Score 31.8; DB 7; Length 1421;

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US-09-925-065A-719738
Query Match      19.9%; Score 31.6; DB 4; Length 812;
Best Local Similarity 52.8%; Pred. No. 48;
Matches 49; Conservative 0; Mismatches 29; Indels 0; Gaps 0;

Qy 65 AACAAAGCAGCTCAAAAGCTACAGAACTCTATTATCAATTTCTGCTCATCTTAATATGTC 124
Db 637 AACCAAAAGGATAAAAGCTTGAGGGATGGATACCTCATTTCTGCTCATGATTAATTC 578

Qy 125 TCTTGCTGATCTGTATCA 142
Db 577 ACATTGTGTGCTGTATCA 560

US-09-925-065A-255686/c
; Sequence 255686, Application US/09925065A
; Publication No. US20050228172A9
; GENERAL INFORMATION:
; APPLICANT: Wang, David G.
; TITLE OF INVENTION: Identification and Mapping of Single
; Nucleotide Polymorphisms in the Human Genome
; FILE REFERENCE: 108827.135
; CURRENT APPLICATION NUMBER: US/09/925,065A
; CURRENT FILING DATE: 2001-08-08
; PRIOR APPLICATION NUMBER: US 60/243,096
; PRIOR FILING DATE: 2000-10-24
; PRIOR APPLICATION NUMBER: US 60/252,147
; PRIOR FILING DATE: 2000-11-20
; PRIOR APPLICATION NUMBER: US 60/250,092
; PRIOR FILING DATE: 2000-11-30
; PRIOR APPLICATION NUMBER: US 60/261,766
; PRIOR FILING DATE: 2001-01-16
; PRIOR APPLICATION NUMBER: US 60/289,846
; PRIOR FILING DATE: 2001-05-09
; NUMBER OF SEQ ID NOS: 957086
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 255686
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-925-065A-255686

Query Match      19.7%; Score 31.4; DB 4; Length 519;
Best Local Similarity 57.7%; Pred. No. 46;
Matches 56; Conservative 0; Mismatches 41; Indels 0; Gaps 0;

Qy 4 GAGAAAGTCCAATACCTCAGCTCAGCTATAGAAAGAGCCTCAACCATTTGAATGCCT 63
Db 263 GAAAAAGTCACACAACATCTTAGCACTATTATGAGAACAGCTTTGACCTTGCAACACTT 204

Qy 64 CAACAAGCAGCTCAAAAGCTACAGAACTCTATTATCA 100
Db 203 GAACATGCTCAGAAATCCTCAAGAACTCTGTGAACCA 167

RESULT 36
US-09-925-065A-246839
; Sequence 246839, Application US/09925065A
; Publication No. US20050228172A9
; GENERAL INFORMATION:
; APPLICANT: Wang, David G.
; TITLE OF INVENTION: Identification and Mapping of Single
; Nucleotide Polymorphisms in the Human Genome
; FILE REFERENCE: 108827.135
; CURRENT APPLICATION NUMBER: US/09/925,065A
; CURRENT FILING DATE: 2001-08-08
; PRIOR APPLICATION NUMBER: US 60/243,096
; PRIOR FILING DATE: 2000-10-24
; PRIOR APPLICATION NUMBER: US 60/252,147
; PRIOR FILING DATE: 2000-11-20
; PRIOR APPLICATION NUMBER: US 60/250,092
; PRIOR FILING DATE: 2000-11-30
; PRIOR APPLICATION NUMBER: US 60/261,766
; PRIOR FILING DATE: 2001-01-16
; PRIOR APPLICATION NUMBER: US 60/289,846
; PRIOR FILING DATE: 2001-05-09
; NUMBER OF SEQ ID NOS: 957086
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 246839
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-925-065A-246839

Query Match      19.7%; Score 31.4; DB 4; Length 519;
Best Local Similarity 57.7%; Pred. No. 46;
Matches 56; Conservative 0; Mismatches 41; Indels 0; Gaps 0;

Qy 4 GAGAAAGTCCAATACCTCAGCTCAGCTATAGAAAGAGCCTCAACCATTTGAATGCCT 63
Db 263 GAAAAAGTCACACAACATCTTAGCACTATTATGAGAACAGCTTTGACCTTGCAACACTT 204

Qy 64 CAACAAGCAGCTCAAAAGCTACAGAACTCTATTATCA 100
Db 203 GAACATGCTCAGAAATCCTCAAGAACTCTGTGAACCA 167

RESULT 37
US-09-925-065A-255687/c
; Sequence 255687, Application US/09925065A
; Publication No. US20050228172A9
; GENERAL INFORMATION:
; APPLICANT: Wang, David G.
; TITLE OF INVENTION: Identification and Mapping of Single
; Nucleotide Polymorphisms in the Human Genome
; FILE REFERENCE: 108827.135
; CURRENT APPLICATION NUMBER: US/09/925,065A
; CURRENT FILING DATE: 2001-08-08
; PRIOR APPLICATION NUMBER: US 60/243,096
; PRIOR FILING DATE: 2000-10-24
; PRIOR APPLICATION NUMBER: US 60/252,147
; PRIOR FILING DATE: 2000-11-20
; PRIOR APPLICATION NUMBER: US 60/250,092
```

APPLICANT: Hyseq, Inc
TITLE OF INVENTION: NOVEL NUCLEIC ACIDS AND POLYPEPTIDES
FILE REFERENCE: 790CIP3/US
CURRENT APPLICATION NUMBER: US/10/450,763
CURRENT FILING DATE: 2003-06-11
PRIOR APPLICATION NUMBER: PCT/US01/08631
PRIOR FILING DATE: 2001-03-30
PRIOR APPLICATION NUMBER: 09/540,217
PRIOR FILING DATE: 2000-03-31
PRIOR APPLICATION NUMBER: 09/649,167
PRIOR FILING DATE: 2000-08-23
NUMBER OF SEQ ID NOS: 60736
SOFTWARE: Custom
SEQ ID NO 5048
LENGTH: 873
TYPE: DNA
ORGANISM: Homo sapiens
FEATURE:
NAME/KEY: SIMILAR
LOCATION: (37)..(153)
OTHER INFORMATION: 97% homologous to Arabidopsis thaliana putative
OTHER INFORMATION: protein, accession number AL162506, Smith-Waterman Score=193.
US-10-450-763-5048

Query Match 19.7%; Score 31.4; DB 9; Length 873;
Best Local Similarity 53.7%; Pred. No. 57;
Matches 65; Conservative 0; Mismatches 56; Indels 0; Gaps 0;
QY 37 AGAAGAGCTCAACCATTTGAATGCTCAACAGCAGCTCAAGAGCTCAAGATCTATTT 96
DB 207 AAAGAAACATACCATTAATAAATTCATATAGGTATTAATAATCTTCCCAAAATCATC 148
QY 97 ATCAATTTCTGTCTCATCTTAATATGCTCTTGTGATCTGTATCATCGTGATGCTTCTC 156
DB 147 TTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTC 88
QY 157 T 157
DB 87 T 87

RESULT 40
US-10-450-763-5355/c
Sequence 5355, Application US/10450763
Publication No. US20050196754A1
GENERAL INFORMATION:
APPLICANT: Hyseq, Inc
TITLE OF INVENTION: NOVEL NUCLEIC ACIDS AND POLYPEPTIDES
FILE REFERENCE: 790CIP3/US
CURRENT APPLICATION NUMBER: US/10/450,763
CURRENT FILING DATE: 2003-06-11
PRIOR APPLICATION NUMBER: PCT/US01/08631
PRIOR FILING DATE: 2001-03-30
PRIOR APPLICATION NUMBER: 09/540,217
PRIOR FILING DATE: 2000-03-31
PRIOR APPLICATION NUMBER: 09/649,167
PRIOR FILING DATE: 2000-08-23
NUMBER OF SEQ ID NOS: 60736
SOFTWARE: Custom
SEQ ID NO 5355
LENGTH: 873
TYPE: DNA
ORGANISM: Homo sapiens
FEATURE:
NAME/KEY: SIMILAR
LOCATION: (37)..(153)
OTHER INFORMATION: 97% homologous to Arabidopsis thaliana putative
OTHER INFORMATION: protein, accession number AL162506, Smith-Waterman Score=193.
US-10-450-763-5355

Query Match 19.7%; Score 31.4; DB 9; Length 873;
Best Local Similarity 53.7%; Pred. No. 57;
Matches 65; Conservative 0; Mismatches 56; Indels 0; Gaps 0;

QY 37 AGAAGAGCTCAACCATTTGAATGCTCAACAGCAGCTCAAGAGCTCAAGATCTATTT 96
DB 207 AAAGAAACATACCATTAATAAATTCATATAGGTATTAATAATCTTCCCAAAATCATC 148
QY 97 ATCAATTTCTGTCTCATCTTAATATGCTCTTGTGATCTGTATCATCGTGATGCTTCTC 156
DB 147 TTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTC 88
QY 157 T 157
DB 87 T 87

RESULT 41
US-10-450-763-11273/c
Sequence 11273, Application US/10450763
Publication No. US20050196754A1
GENERAL INFORMATION:
APPLICANT: Hyseq, Inc
TITLE OF INVENTION: NOVEL NUCLEIC ACIDS AND POLYPEPTIDES
FILE REFERENCE: 790CIP3/US
CURRENT APPLICATION NUMBER: US/10/450,763
CURRENT FILING DATE: 2003-06-11
PRIOR APPLICATION NUMBER: PCT/US01/08631
PRIOR FILING DATE: 2001-03-30
PRIOR APPLICATION NUMBER: 09/540,217
PRIOR FILING DATE: 2000-03-31
PRIOR APPLICATION NUMBER: 09/649,167
PRIOR FILING DATE: 2000-08-23
NUMBER OF SEQ ID NOS: 60736
SOFTWARE: Custom
SEQ ID NO 11273
LENGTH: 873
TYPE: DNA
ORGANISM: Homo sapiens
FEATURE:
NAME/KEY: SIMILAR
LOCATION: (361)..(948)
OTHER INFORMATION: 87% homologous to Homo sapiens putative p150, accession number
OTHER INFORMATION: U93563, Smith-Waterman Score=845.
US-10-450-763-11273

Query Match 19.7%; Score 31.4; DB 9; Length 873;
Best Local Similarity 53.7%; Pred. No. 57;
Matches 65; Conservative 0; Mismatches 56; Indels 0; Gaps 0;

QY 37 AGAAGAGCTCAACCATTTGAATGCTCAACAGCAGCTCAAGAGCTCAAGATCTATTT 96
DB 207 AAAGAAACATACCATTAATAAATTCATATAGGTATTAATAATCTTCCCAAAATCATC 148
QY 97 ATCAATTTCTGTCTCATCTTAATATGCTCTTGTGATCTGTATCATCGTGATGCTTCTC 156
DB 147 TTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTC 88
QY 157 T 157
DB 87 T 87

RESULT 42
US-10-437-963-88801/c
Sequence 88801, Application US/10437963
Publication No. US20040123343A1
GENERAL INFORMATION:
APPLICANT: La Rosa, Thomas J.
APPLICANT: Kovalic, David K.
APPLICANT: Zhou, Yihua
APPLICANT: Cao, Yongwei
APPLICANT: Wu, Wei
APPLICANT: Boukharov, Andrey A.
APPLICANT: Barbazuk, Brad
APPLICANT: Li, Ping

Db 1860510 TGCCACTAAAGGAATTCAGTAACATCCAAAATTCATGCTGTATGATGCTGTGCTCTTAA 1860451
QY 119 TATGTCCTCTGCTGATCTGTATCATCGTG 147
Db 1860450 TATGGGCTTTGTGTCAGTCTAGATCATTTTG 1860422
RESULT 47
US-10-424-599-49155
; Sequence 49155, Application US/10424599
; Publication No. US20040031072A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa Thomas J
; APPLICANT: Kovalic David K
; APPLICANT: Zhou Yihua
; APPLICANT: Cao Yongwei
; TITLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules Associated With
; FILE OF INVENTION: Plants and Uses Thereof for Plant Improvement
; FILE REFERENCE: 38-21(53223)B
; CURRENT APPLICATION NUMBER: US/10/424,599
; CURRENT FILING DATE: 2003-04-28
; NUMBER OF SEQ ID NOS: 285684
; SEQ ID NO 49155
; LENGTH: 453
; TYPE: DNA
; ORGANISM: Glycine max
; FEATURE:
; OTHER INFORMATION: Clone ID: PAT_MRT3847_15395C.1
; US-10-424-599-49155
Query Match 19.6%; Score 31.2; DB 7; Length 453;
Best Local Similarity 66.2%; Pred. No. 50;
Matches 45; Conservative 0; Mismatches 23; Indels 0; Gaps 0;
QY 92 TATTATCAATTTCTGTCATCTTAATATGTCCTTCTGTCATCTGTATCATCGTGATGC 151
Db 22 TATTAGGTATTACTCTCTCATTTTACATGTCATCTCTAGTGGTCTCATTAATTAATC 81
QY 152 TTCTCTGA 159
Db 82 TCTTCTTA 89
RESULT 48
US-10-087-192-712/c
; Sequence 712, Application US/10087192
; Publication No. US20020182586A1
; GENERAL INFORMATION:
; APPLICANT: Morris, David W.
; APPLICANT: Engelhard, Eric K.
; TITLE OF INVENTION: NOVEL COMPOSITIONS AND METHODS FOR
; FILE OF INVENTION: CANCER
; FILE REFERENCE: 529452000122
; CURRENT APPLICATION NUMBER: US/10/087,192
; CURRENT FILING DATE: 2002-03-01
; PRIOR APPLICATION NUMBER: US 09/747,377
; PRIOR FILING DATE: 2000-12-22
; PRIOR APPLICATION NUMBER: US 09/798,586
; PRIOR FILING DATE: 2001-03-02
; NUMBER OF SEQ ID NOS: 2059
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 712
; LENGTH: 84073
; TYPE: DNA
; ORGANISM: Homo sapiens
; US-10-087-192-712
Query Match 19.6%; Score 31.2; DB 5; Length 84073;
Best Local Similarity 58.7%; Pred. No. 4.3e+02;
Matches 54; Conservative 0; Mismatches 38; Indels 0; Gaps 0;
QY 37 AGAGAGCTCAACCATTTGAATGCTCAACAGCAGCTCAAAAGCTACAGATCTATT 96

US-10-091-412-1-1.npbbm
; PRIOR FILING DATE: 1999-11-23
; PRIOR APPLICATION NUMBER: US 60/156,358
; PRIOR FILING DATE: 1999-09-28
; PRIOR APPLICATION NUMBER: US 60/146,002
; PRIOR FILING DATE: 1999-08-09
; NUMBER OF SEQ ID NOS: 325720
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 174763
; LENGTH: 2940917
; TYPE: DNA
; ORGANISM: Human
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (1)-(2940917)
; OTHER INFORMATION: n = A,T,C or G
US-10-027-632-174763
Query Match 19.7%; Score 31.4; DB 5; Length 2940917;
Best Local Similarity 59.6%; Pred. No. 1.2e+03;
Matches 53; Conservative 0; Mismatches 36; Indels 0; Gaps 0;
QY 59 TGCTCAACAGCAGTCAAGCTACAGATCTATTATCAATTTCTGTCATCTTAA 118
Db 1860510 TGCCACTAAAGGAATTCAGTAACATCCAAAATTCATGCTGTATGATGCTGTGCTCTTAA 1860451
QY 119 TATGTCCTCTGCTGATCTGTATCATCGTG 147
Db 1860450 TATGGGCTTTGTGTCAGTCTAGATCATTTTG 1860422
RESULT 46
US-10-027-632-174763/c
; Sequence 174763, Application US/10027632
; Publication No. US20030204075A9
; GENERAL INFORMATION:
; APPLICANT: Wang, David G.
; TITLE OF INVENTION: Identification and Mapping of Single Nucleotide
; FILE OF INVENTION: Polymorphisms in the Human Genome
; FILE REFERENCE: 108827.129
; CURRENT APPLICATION NUMBER: US/10/027,632
; CURRENT FILING DATE: 2002-04-30
; PRIOR APPLICATION NUMBER: US 60/218,006
; PRIOR FILING DATE: 2000-07-12
; PRIOR APPLICATION NUMBER: US 60/198,676
; PRIOR FILING DATE: 2000-04-20
; PRIOR APPLICATION NUMBER: US 60/193,483
; PRIOR FILING DATE: 2000-03-29
; PRIOR APPLICATION NUMBER: US 60/185,218
; PRIOR FILING DATE: 2000-02-24
; PRIOR APPLICATION NUMBER: US 60/167,363
; PRIOR FILING DATE: 1999-11-23
; PRIOR APPLICATION NUMBER: US 60/156,358
; PRIOR FILING DATE: 1999-09-28
; PRIOR APPLICATION NUMBER: US 60/146,002
; PRIOR FILING DATE: 1999-08-09
; NUMBER OF SEQ ID NOS: 325720
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 174763
; LENGTH: 2940917
; TYPE: DNA
; ORGANISM: Human
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (1)-(2940917)
; OTHER INFORMATION: n = A,T,C or G
US-10-027-632-174763
Query Match 19.7%; Score 31.4; DB 6; Length 2940917;
Best Local Similarity 59.6%; Pred. No. 1.2e+03;
Matches 53; Conservative 0; Mismatches 36; Indels 0; Gaps 0;
QY 59 TGCTCAACAGCAGTCAAGCTACAGATCTATTATCAATTTCTGTCATCTTAA 118

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Db      28668 AGTAGAGATACAGCCACACAAAAGAAATCCAGGGTCACATAAAACCAACAGAAAGTTATCT 28609
QY      97 ATCAATTTCTGTCATCTTAATATGTCCTT 128
Db      28608 AACCAACCTTTGAATCTTGTAAATCTGAGTCTT 28577

RESULT 49
US-10-027-632-233567/c
; Sequence 233567, Application US/10027632
; Publication No. US20020198371A1
; GENERAL INFORMATION:
; APPLICANT: Wang, David G.
; TITLE OF INVENTION: Identification and Mapping of Single Nucleotide
; POLYMORPHISMS IN THE HUMAN GENOME
; FILE REFERENCE: 108827.129
; CURRENT APPLICATION NUMBER: US/10/027,632
; CURRENT FILING DATE: 2002-04-30
; PRIOR APPLICATION NUMBER: US 60/218,006
; PRIOR FILING DATE: 2000-07-12
; PRIOR APPLICATION NUMBER: US 60/198,676
; PRIOR FILING DATE: 2000-04-20
; PRIOR APPLICATION NUMBER: US 60/193,483
; PRIOR FILING DATE: 2000-03-29
; PRIOR APPLICATION NUMBER: US 60/185,218
; PRIOR FILING DATE: 2000-02-24
; PRIOR APPLICATION NUMBER: US 60/167,363
; PRIOR FILING DATE: 1999-11-23
; PRIOR APPLICATION NUMBER: US 60/156,358
; PRIOR FILING DATE: 1999-09-28
; PRIOR APPLICATION NUMBER: US 60/146,002
; PRIOR FILING DATE: 1999-08-09
; NUMBER OF SEQ ID NOS: 325720
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 233567
; LENGTH: 633
; TYPE: DNA
; ORGANISM: Human
US-10-027-632-233567

      Query Match      19.5%; Score 31; DB 5; Length 633;
      Best Local Similarity 72.7%; Pred. No. 66;
      Matches 40; Conservative 0; Mismatches 15; Indels 0; Gaps 0;

QY      89 ATCTATTATCAATTTCTGTCATCTTAATATGTCCTTGTGATCTGTATCAT 143
Db      178 ATATAATTATATATTGATGATCATCATATTTATCTATCATCTACTCTGTATGAT 124

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Job time : 819 secs
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; PRIOR FILING DATE: 1999-08-09
; NUMBER OF SEQ ID NOS: 325720
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 233567
; LENGTH: 633
; TYPE: DNA
; ORGANISM: Human
US-10-027-632-233567

      Query Match      19.5%; Score 31; DB 6; Length 633;
      Best Local Similarity 72.7%; Pred. No. 66;
      Matches 40; Conservative 0; Mismatches 15; Indels 0; Gaps 0;

QY      89 ATCTATTATCAATTTCTGTCATCTTAATATGTCCTTGTGATCTGTATCAT 143
Db      178 ATATAATTATATATTGATGATCATCATATTTATCTATCATCTACTCTGTATGAT 124

Search completed: December 8, 2005, 04:24:50
Job time : 819 secs
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OM nucleic - nucleic search, using sw model

Run on: December 8, 2005, 02:14:01 ; Search time 648 Seconds

Title: US-10-691-412-1
Perfect score: 159
Sequence: 1 atggagaaagtccaatacct.....tcacgtgatgtctctga 159
(without alignments)
91.733 Million cell updates/sec

Scoring table: IDENTITY NUC

Gapop 10.0 , Gapext 1.0

Searched: 3392430 seqs, 186927314 residues

Total number of hits satisfying chosen parameters: 6784860

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 100 summaries

Database : Published Applications NA New:*

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- 2: /cgn2_6/ptodata/1/pubpna/US06_NEW_PUB.seq:*
- 3: /cgn2_6/ptodata/1/pubpna/US07_NEW_PUB.seq:*
- 4: /cgn2_6/ptodata/1/pubpna/US08_NEW_PUB.seq:*
- 5: /cgn2_6/ptodata/1/pubpna/PCT_NEW_PUB.seq:*
- 6: /cgn2_6/ptodata/1/pubpna/US10_NEW_PUB.seq:*
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- 9: /cgn2_6/ptodata/1/pubpna/US11_NEW_PUB.seq:*
- 10: /cgn2_6/ptodata/1/pubpna/US60_NEW_PUB.seq:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	31.8	20.0	150038	7	US-11-121-086-23
2	31.4	19.7	1844	6	US-10-750-185-64456
3	31	19.5	1256	6	US-10-750-185-48336
4	30.2	19.0	958	6	US-10-750-185-44270
5	29	18.2	172147	7	US-11-112-908-22
6	29	18.2	188682	7	US-11-112-908-33
7	28.8	18.1	193363	7	US-11-112-908-32
8	28.4	17.9	2618	6	US-10-750-185-42442
9	28.2	17.7	1005	6	US-10-750-185-42220
10	28.2	17.7	1025	6	US-10-750-185-32974
11	27.8	17.5	600	6	US-10-750-185-917
12	27.8	17.5	1327	6	US-10-750-185-60655
13	27.6	17.4	738	6	US-10-750-185-52599
14	27.6	17.4	744	6	US-10-750-185-54343
15	27.6	17.4	1301	6	US-10-750-185-26340
16	27.6	17.4	1749	6	US-10-750-185-1079
17	27.6	17.4	3105	6	US-10-750-185-4436
18	27.4	17.2	1183	6	US-10-750-185-51145
19	27.4	17.2	1305	6	US-10-750-185-51810
20	27.4	17.2	2317	6	US-10-750-185-59493
21	27.4	17.2	2563	6	US-10-750-185-37324
22	27.4	17.2	156544	7	US-11-121-086-81
23	27.4	17.2	170837	7	US-11-121-086-97

24	27.4	17.2	171423	7	US-11-121-086-85	Sequence 85, Appl
c 25	27.2	17.1	666	6	US-10-793-626-2777	Sequence 2777, Ap
26	27.2	17.1	864	6	US-10-750-185-52881	Sequence 52881, A
27	27.2	17.1	4136	6	US-10-793-626-3686	Sequence 3686, Ap
c 28	27.2	17.1	196200	7	US-11-121-086-9	Sequence 9, Appli
c 29	27.2	17.1	246960	7	US-11-121-086-8	Sequence 8, Appli
c 30	27.2	17.1	319608	7	US-11-145-703-1	Sequence 1, Appli
31	27	17.0	742	6	US-10-793-626-2981	Sequence 2981, Ap
c 32	27	17.0	2116	6	US-10-750-185-36690	Sequence 36690, A
c 33	27	17.0	2332	6	US-10-750-185-57047	Sequence 57047, A
c 34	27	17.0	2744	6	US-10-750-185-30659	Sequence 30659, A
c 35	27	17.0	3048	6	US-10-793-626-3660	Sequence 3660, Ap
36	27	17.0	3163	6	US-10-793-626-3889	Sequence 3889, Ap
37	27	17.0	4113	6	US-10-624-932-21	Sequence 21, Appli
38	27	17.0	5855	7	US-11-108-528-27	Sequence 27, Appl
39	27	17.0	212805	7	US-11-112-908-19	Sequence 19, Appl
c 40	26.8	16.9	1229	6	US-10-750-185-26323	Sequence 26323, A
41	26.8	16.9	1320	6	US-10-750-185-55086	Sequence 55086, A
42	26.8	16.9	1733	6	US-10-750-185-33223	Sequence 33223, A
c 43	26.8	16.9	3617	6	US-10-131-826A-409	Sequence 409, App
c 44	26.8	16.9	3627	6	US-10-750-185-35364	Sequence 35364, A
c 45	26.8	16.9	138821	7	US-11-121-086-80	Sequence 80, Appl
c 46	26.8	16.9	139054	7	US-11-121-086-96	Sequence 96, Appl
47	26.8	16.9	156735	7	US-11-121-086-93	Sequence 93, Appl
c 48	26.6	16.7	847	6	US-10-750-185-32215	Sequence 32215, A
c 49	26.6	16.7	1197	7	US-11-112-908-135	Sequence 135, App
c 50	26.6	16.7	1256	6	US-10-750-185-30040	Sequence 30040, A
c 51	26.6	16.7	1524	6	US-10-750-185-47853	Sequence 47853, A
52	26.6	16.7	1573	6	US-10-750-185-55695	Sequence 55695, A
c 53	26.6	16.7	2057	6	US-10-750-185-60135	Sequence 60135, A
c 54	26.6	16.7	2079	6	US-10-750-185-52763	Sequence 52763, A
55	26.6	16.7	2915	6	US-10-750-185-49578	Sequence 49578, A
56	26.6	16.7	3040	6	US-10-793-626-3789	Sequence 3789, Ap
57	26.6	16.7	3204	6	US-10-793-626-4294	Sequence 4294, Ap
58	26.6	16.7	3994	6	US-10-750-185-32760	Sequence 3496, Ap
c 59	26.6	16.7	4605	6	US-11-112-908-40	Sequence 40, Appl
c 60	26.6	16.7	180862	7	US-11-121-086-50	Sequence 50, Appl
61	26.6	16.7	190882	7	US-11-121-086-69	Sequence 69, Appl
c 62	26.6	16.7	203457	7	US-11-121-086-50	Sequence 50, Appl
c 63	26.4	16.6	1672	6	US-10-750-185-60433	Sequence 60433, A
c 64	26.4	16.6	2016	6	US-10-750-185-46930	Sequence 46930, A
c 65	26.4	16.6	159497	7	US-11-112-908-61	Sequence 61, Appl
c 66	26.4	16.6	162173	7	US-11-121-086-72	Sequence 72, Appl
c 67	26.4	16.6	185393	7	US-11-121-086-101	Sequence 101, App
c 68	26.2	16.5	600	6	US-10-750-185-2944	Sequence 2944, Ap
69	26.2	16.5	1008	6	US-10-750-185-62885	Sequence 62885, A
70	26.2	16.5	1546	6	US-10-750-185-32954	Sequence 32954, A
c 71	26.2	16.5	1557	7	US-11-133-345-100	Sequence 100, App
c 72	26.2	16.5	1751	6	US-10-750-185-27624	Sequence 27624, A
c 73	26.2	16.5	2271	6	US-10-750-185-59933	Sequence 59933, A
c 74	26.2	16.5	3331	7	US-11-000-463-8	Sequence 8, Appli
c 75	26.2	16.5	3690	7	US-11-000-463-480	Sequence 480, App
c 76	26.2	16.5	85682	7	US-11-117-187-205	Sequence 205, App
c 77	26.2	16.5	163317	7	US-11-117-187-212	Sequence 212, App
c 78	26.2	16.5	165627	7	US-11-121-086-89	Sequence 89, Appl
c 79	26.2	16.5	176503	7	US-11-121-086-53	Sequence 53, Appl
c 80	26.2	16.5	611587	7	US-11-117-187-209	Sequence 209, App
c 81	26	16.4	1253	6	US-10-750-185-35340	Sequence 35340, A
c 82	26	16.4	1461	6	US-10-750-185-53487	Sequence 53487, A
c 83	26	16.4	1577	6	US-10-750-185-45716	Sequence 45716, A
c 84	26	16.4	1613	6	US-10-750-185-41450	Sequence 41450, A
c 85	26	16.4	3198	6	US-11-054-385-11	Sequence 11, Appl
c 86	26	16.4	150468	7	US-10-750-185-63042	Sequence 63042, A
87	26	16.4	3730	6	US-10-485-517-116	Sequence 116, App
c 88	26	16.4	150468	7	US-11-112-908-56	Sequence 56, Appl
c 89	26	16.4	151828	7	US-11-117-187-197	Sequence 197, App
c 90	26	16.4	172781	7	US-11-112-908-25	Sequence 25, Appl
c 91	26	16.4	177175	7	US-11-121-086-79	Sequence 79, Appl
c 92	26	16.4	179777	7	US-11-121-086-106	Sequence 106, App
c 93	26	16.4	193789	7	US-11-112-908-55	Sequence 55, Appl
c 94	26	16.4	235033	7	US-11-157-389-1	Sequence 1, Appli
c 95	26	16.4	237326	7	US-11-157-389-2	Sequence 2, Appli
c 96	26	16.4	260209	6	US-10-933-025-23	Sequence 23, Appl

c 97 25.8 16.2 600 6 US-10-750-185-3836 Sequence 3836, Ap
c 98 25.8 16.2 600 6 US-10-750-185-20094 Sequence 20094, A
c 99 25.8 16.2 600 6 US-10-750-185-21310 Sequence 21310, A
c 100 25.8 16.2 743 6 US-10-750-185-31770 Sequence 31770, A

ALIGNMENTS

RESULT 1
US-11-121-086-23
; Sequence 23, Application US/11121086
; Publication No. US20050266459A1
; GENERAL INFORMATION:
; APPLICANT: POULSEN, TIM S.
; APPLICANT: NIELSEN, KIRSTEN V.
; TITLE OF INVENTION: NUCLEIC ACID PROBES AND NUCLEIC ACID ANALOG PROBES
; FILE REFERENCE: 09138.6000-0000
; CURRENT APPLICATION NUMBER: US/11/121,086
; CURRENT FILING DATE: 2005-05-04
; PRIOR APPLICATION NUMBER: 60/567,570
; PRIOR FILING DATE: 2004-05-04
; NUMBER OF SEQ ID NOS: 107
; SOFTWARE: Patentin version 3.3
; SEQ ID NO 23
; LENGTH: 150038
; TYPE: DNA
; ORGANISM: Homo sapiens
US-11-121-086-23

Query Match 20.0%; Score 31.8; DB 7; Length 150038;
Best Local Similarity 54.8%; Pred. No. 8.2; Indels 0; Gaps 0;
Matches 63; Conservative 0; Mismatches 52

QY 34 ATAAGAGAGCCTCAACCATTTGAATGCTCAACAGCAGCTCAAAAGCTACAGATCTTA 93
DB 10677 ATCAAAACAGCATTAACAGTAACAGGTTTCAAGCTTTCTACATGCACACTTACACA 10736

QY 94 TTATCAATTTCTGCTCATCTTAAATATGCTCTTCTGCTGATCGTATCATCGTGA 148
DB 10737 ATTATCCCTTAATTTTATCTTCATATATATATGATGATCTATTTGTTCTGA 10791

RESULT 2
US-10-750-185-64456/c
; Sequence 64456, Application US/10750185
; Publication No. US20050260603A1
; GENERAL INFORMATION:
; APPLICANT: MMI GENOMICS, INC.
; APPLICANT: DENISE, Sue K.
; APPLICANT: KERR, Richard
; APPLICANT: ROSENFELD, David
; APPLICANT: HOLM, Tom
; APPLICANT: BATES, Stephen
; APPLICANT: FANTIN, Dennis
; TITLE OF INVENTION: COMPOSITIONS FOR INFERRING BOVINE TRAITS
; FILE REFERENCE: MM1100-2
; CURRENT APPLICATION NUMBER: US/10/750,185
; CURRENT FILING DATE: 2003-12-31
; PRIOR APPLICATION NUMBER: US 60/437,482
; PRIOR FILING DATE: 2002-12-31
; NUMBER OF SEQ ID NOS: 64922
; SOFTWARE: Patentin version 3.1
; SEQ ID NO 64456
; LENGTH: 1844
; TYPE: DNA
; ORGANISM: Bovine 19866880659967
US-10-750-185-64456

Query Match 19.7%; Score 31.4; DB 6; Length 1844;
Best Local Similarity 59.6%; Pred. No. 2.4; Indels 0; Gaps 0;
Matches 53; Conservative 0; Mismatches 36

QY 38 GAAGAGCCTCAACCATTTGAATGCTCAACAGCAGCTCAAAAGCTACAGATCTTATTA 97
DB 128 GACAGGACTGAGCGACTGAACAATAACAAAGTAATTAACAAGACCAACTGTCTCTATTA 69
QY 98 TCAATTTCTGCTCATCTTAAATATGCTC 126
DB 68 TGAATTAATTTCTTAACCTTCGTAITCCAC 40

RESULT 3
US-10-750-185-48936/c
; Sequence 48936, Application US/10750185
; Publication No. US20050260603A1
; GENERAL INFORMATION:
; APPLICANT: MMI GENOMICS, INC.
; APPLICANT: DENISE, Sue K.
; APPLICANT: KERR, Richard
; APPLICANT: ROSENFELD, David
; APPLICANT: HOLM, Tom
; APPLICANT: BATES, Stephen
; APPLICANT: FANTIN, Dennis
; TITLE OF INVENTION: COMPOSITIONS FOR INFERRING BOVINE TRAITS
; FILE REFERENCE: MM1100-2
; CURRENT APPLICATION NUMBER: US/10/750,185
; CURRENT FILING DATE: 2003-12-31
; PRIOR APPLICATION NUMBER: US 60/437,482
; PRIOR FILING DATE: 2002-12-31
; NUMBER OF SEQ ID NOS: 64922
; SOFTWARE: Patentin version 3.1
; SEQ ID NO 48936
; LENGTH: 1256
; TYPE: DNA
; ORGANISM: Bovine 19866880996475
US-10-750-185-48936

Query Match 19.5%; Score 31; DB 6; Length 1256;
Best Local Similarity 72.7%; Pred. No. 2.8; Indels 0; Gaps 0;
Matches 40; Conservative 0; Mismatches 15

QY 104 TCTGCTCATCTTAATATGCTCTTCTGCTGATCTGATCATCGTATCGTGTCTGTG 158
DB 68 TCTGCCACAGACTAATATGTAATCTTCTTCTTCATCATAGTATGATGATCTGTG 14

RESULT 4
US-10-750-185-44270
; Sequence 44270, Application US/10750185
; Publication No. US20050260603A1
; GENERAL INFORMATION:
; APPLICANT: MMI GENOMICS, INC.
; APPLICANT: DENISE, Sue K.
; APPLICANT: KERR, Richard
; APPLICANT: ROSENFELD, David
; APPLICANT: HOLM, Tom
; APPLICANT: BATES, Stephen
; APPLICANT: FANTIN, Dennis
; TITLE OF INVENTION: COMPOSITIONS FOR INFERRING BOVINE TRAITS
; FILE REFERENCE: MM1100-2
; CURRENT APPLICATION NUMBER: US/10/750,185
; CURRENT FILING DATE: 2003-12-31
; PRIOR APPLICATION NUMBER: US 60/437,482
; PRIOR FILING DATE: 2002-12-31
; NUMBER OF SEQ ID NOS: 64922
; SOFTWARE: Patentin version 3.1
; SEQ ID NO 44270
; LENGTH: 958
; TYPE: DNA
; ORGANISM: Bovine 19866881864870
US-10-750-185-44270

Query Match 19.0%; Score 30.2; DB 6; Length 958;
Best Local Similarity 58.2%; Pred. No. 4.4; Indels 0; Gaps 0;
Matches 53; Conservative 0; Mismatches 38

QY 51 CATTGAATGCTCAACAGCAGCTCAAAAGCTACAGAACTATTATTAATCAATTTCTGTCT 110
Db 834 CATTGATATTTCTCATTGAACAACTTTTACACACTTGAGAAATTATAGTGGAATGTGTGT 893
QY 111 CATCTTAATATGCTCTTCTGCTGATCTGATC 141
Db 894 AAATGAAGAAGTCCCGAAGTCTTTTACC 924

RESULT 5
US-11-112-908-22
; Sequence 22, Application US/11112908
; Publication No. US20050260659A1
; GENERAL INFORMATION:
; APPLICANT: Harris, Cole
; TITLE OF INVENTION: Breast Cancer Biomarkers
; FILE REFERENCE: 04-164-US
; CURRENT APPLICATION NUMBER: US/11/112,908
; PRIOR FILING DATE: 2005-04-22
; PRIOR APPLICATION NUMBER: US 60/564,758
; PRIOR FILING DATE: 2004-04-23
; PRIOR APPLICATION NUMBER: US 60/575,978
; PRIOR FILING DATE: 2004-06-01
; PRIOR APPLICATION NUMBER: US 60/631,702
; PRIOR FILING DATE: 2004-11-30
; PRIOR APPLICATION NUMBER: US 60/633,826
; PRIOR FILING DATE: 2004-12-07
; NUMBER OF SEQ ID NOS: 511
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 22
; LENGTH: 172147
; TYPE: DNA
; ORGANISM: Homo sapiens
US-11-112-908-22

Query Match 18.2%; Score 29; DB 7; Length 172147;
Best Local Similarity 53.0%; Pred. No. 58;
Matches 62; Conservative 0; Mismatches 55; Indels 0; Gaps 0;
QY 10 GTCCATACCTCACTCGCTCAGCTATTAAGAGAGCCTCAACAACTGAAATGCTCAACAA 69
Db 140767 GTGAACCTGACCTGCTCAAACTGGTGTAGCAAAATCAACAAATTTGTTGCAACACAG 140826
QY 70 GCAGGTCAAAAGCTACAGAACTATTATTAATCAATTTCTGCTCATCTTAATATGCTC 126
Db 140827 CAACAACACACAAAGAAATCTTTTTTTTTTTTGTGAGTCTTGTCTGTCTAC 140883

RESULT 6
US-11-112-908-23
; Sequence 23, Application US/11112908
; Publication No. US20050260659A1
; GENERAL INFORMATION:
; APPLICANT: Harris, Cole
; TITLE OF INVENTION: Breast Cancer Biomarkers
; FILE REFERENCE: 04-164-US
; CURRENT APPLICATION NUMBER: US/11/112,908
; PRIOR FILING DATE: 2005-04-22
; PRIOR APPLICATION NUMBER: US 60/564,758
; PRIOR FILING DATE: 2004-04-23
; PRIOR APPLICATION NUMBER: US 60/575,978
; PRIOR FILING DATE: 2004-06-01
; PRIOR APPLICATION NUMBER: US 60/631,702
; PRIOR FILING DATE: 2004-11-30
; PRIOR APPLICATION NUMBER: US 60/633,826
; PRIOR FILING DATE: 2004-12-07
; NUMBER OF SEQ ID NOS: 511
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 23
; LENGTH: 188682

; TYPE: DNA
; ORGANISM: Homo sapiens
US-11-112-908-23
Query Match 18.2%; Score 29; DB 7; Length 188682;
Best Local Similarity 53.0%; Pred. No. 59;
Matches 62; Conservative 0; Mismatches 55; Indels 0; Gaps 0;
QY 10 GTCCATACCTCACTCGCTCAGCTATTAAGAGAGCCTCAACAACTGAAATGCTCAACAA 69
Db 90388 GTGAACCTGACCTGCTCAAACTGGTGTAGCAAAATCAACAAATTTGTTGCAACACAG 90447
QY 70 GCAGGTCAAAAGCTACAGAACTATTATTAATCAATTTCTGCTCATCTTAATATGCTC 126
Db 90448 CAACAACACACAAAGAAATCTTTTTTTTTTTTGTGAGTCTTGTCTGTCTAC 90504

RESULT 7
US-11-112-908-32/c
; Sequence 32, Application US/11112908
; Publication No. US20050260659A1
; GENERAL INFORMATION:
; APPLICANT: Harris, Cole
; TITLE OF INVENTION: Breast Cancer Biomarkers
; FILE REFERENCE: 04-164-US
; CURRENT APPLICATION NUMBER: US/11/112,908
; PRIOR FILING DATE: 2005-04-22
; PRIOR APPLICATION NUMBER: US 60/564,758
; PRIOR FILING DATE: 2004-04-23
; PRIOR APPLICATION NUMBER: US 60/575,978
; PRIOR FILING DATE: 2004-06-01
; PRIOR APPLICATION NUMBER: US 60/631,702
; PRIOR FILING DATE: 2004-11-30
; PRIOR APPLICATION NUMBER: US 60/633,826
; PRIOR FILING DATE: 2004-12-07
; NUMBER OF SEQ ID NOS: 511
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 32
; LENGTH: 193363
; TYPE: DNA
; ORGANISM: Homo sapiens
US-11-112-908-32

Query Match 18.1%; Score 28.8; DB 7; Length 193363;
Best Local Similarity 65.6%; Pred. No. 69;
Matches 42; Conservative 0; Mismatches 22; Indels 0; Gaps 0;
QY 77 AAAAGCTACAGAACTATTATTAATCAATTTCTGCTCATCTTAATATGCTCTTCTGCTGATCT 136
Db 13416 AATAGTCACAGAACTGGTGTATCATCTTTCTCTCTTTCTTTCTTTCTTTCTTTCTGCTCT 13357
QY 137 GTAT 140
Db 13356 TTCT 13353

RESULT 8
US-10-750-185-42442
; Sequence 42442, Application US/10750185
; Publication No. US20050260603A1
; GENERAL INFORMATION:
; APPLICANT: MMI GENOMICS, INC.
; APPLICANT: DENISE, Sue K.
; APPLICANT: KERR, Richard
; APPLICANT: ROSENFELD, David
; APPLICANT: HOLM, Tom
; APPLICANT: BATES, Stephen
; APPLICANT: FANTIN, Dennis
; TITLE OF INVENTION: COMPOSITIONS FOR INFERRING BOVINE TRAITS
; FILE REFERENCE: MM1100-2
; CURRENT APPLICATION NUMBER: US/10/750,185
; CURRENT FILING DATE: 2003-12-31

```
; PRIOR APPLICATION NUMBER: US 60/437,482
; PRIOR FILING DATE: 2002-12-31
; NUMBER OF SEQ ID NOS: 64922
; SOFTWARE: PatentIN version 3.1
; SEQ ID NO 42442
; LENGTH: 2618
; TYPE: DNA
; ORGANISM: Bovine 19866881135702
US-10-750-185-42442

Query Match      17.9%; Score 28.4; DB 6; Length 2618;
Best Local Similarity 54.9%; Pred. No. 21;
Matches 56; Conservative 0; Mismatches 46; Indels 0; Gaps 0;

QY 58 ATGCTCTCAACAGCAGCTCAAAAGCTACAGATCTATTATCAATTTCTGCTCATCTTA 117
Db 2082 ATTCATAAGCAATATTTTCAAAAAATACACAGTACTATTAAACCTATTTTATCACT 2141

QY 118 ATATGCTCTTCTGCTGATCTGATCATCGTGATGCTTCTCTGA 159
Db 2142 TAATGCTCAATGCTTATCGCTTTTGTATTATAAATACGACATGA 2183

RESULT 9
US-10-750-185-42320
; Sequence 42320, Application US/10750185
; Publication No. US20050260603A1
; GENERAL INFORMATION:
; APPLICANT: MMI GENOMICS, INC.
; APPLICANT: DENISE, Sue K.
; APPLICANT: KERR, Richard
; APPLICANT: ROSENFELD, David
; APPLICANT: HOLM, Tom
; APPLICANT: BATES, Stephen
; APPLICANT: FANTIN, Dennis
; TITLE OF INVENTION: COMPOSITIONS FOR INFERRING BOVINE TRAITS
; FILE REFERENCE: MM1100-2
; CURRENT APPLICATION NUMBER: US/10750,185
; CURRENT FILING DATE: 2003-12-31
; PRIOR APPLICATION NUMBER: US 60/437,482
; PRIOR FILING DATE: 2002-12-31
; NUMBER OF SEQ ID NOS: 64922
; SOFTWARE: PatentIN version 3.1
; SEQ ID NO 42320
; LENGTH: 1005
; TYPE: DNA
; ORGANISM: Bovine 19866880600062
US-10-750-185-42320

Query Match      17.7%; Score 28.2; DB 6; Length 1005;
Best Local Similarity 53.1%; Pred. No. 17;
Matches 60; Conservative 0; Mismatches 53; Indels 0; Gaps 0;

QY 39 AAGAGCTCAACCACTTGAATGCTCAACAGCAGCTCAAAAGCTACAGAAATCTATTAT 98
Db 277 AAGAGATGAAGAGAGAGAGAGCTCAAGCAACTTCAAGTTTCGAGCTGTGATGT 336

QY 99 CAATTTCTGCTCATCTTAATATGCTCTTCTGCTGATCTGTATCATCTGTATGC 151
Db 337 AATGGCTCGTCCATGGTGATTTTATTTGGTTTACTTTTATCATCTGTAATGC 389

RESULT 10
US-10-750-185-32974/c
; Sequence 32974, Application US/10750185
; Publication No. US20050260603A1
; GENERAL INFORMATION:
; APPLICANT: MMI GENOMICS, INC.
; APPLICANT: DENISE, Sue K.
; APPLICANT: KERR, Richard
; APPLICANT: ROSENFELD, David
; APPLICANT: HOLM, Tom
; APPLICANT: BATES, Stephen
; TITLE OF INVENTION: COMPOSITIONS FOR INFERRING BOVINE TRAITS
; FILE REFERENCE: MM1100-2
; CURRENT APPLICATION NUMBER: US/10750,185
; CURRENT FILING DATE: 2003-12-31
; PRIOR APPLICATION NUMBER: US 60/437,482
; PRIOR FILING DATE: 2002-12-31
; NUMBER OF SEQ ID NOS: 64922
; SOFTWARE: PatentIN version 3.1
; SEQ ID NO 32974
; LENGTH: 1025
; TYPE: DNA
; ORGANISM: Bovine 19866881951924
US-10-750-185-32974

Query Match      17.7%; Score 28.2; DB 6; Length 1025;
Best Local Similarity 57.3%; Pred. No. 18;
Matches 51; Conservative 0; Mismatches 38; Indels 0; Gaps 0;

QY 64 CAACAGCAGCTCAAAAGCTACAGATCTATTATCAATTTCTGCTCATCTTAATATGT 123
Db 488 CAGCAGCAACCTAATATTATAAAATTTCTATTTCCCAATCTACTACTTAGACAGTTATTCAG 429

QY 124 CTCCTTGCTGATCTGATCATCTGTGATGCT 152
Db 428 TTCCTTACAGATCTGTTTCATCATATTGAT 400

RESULT 11
US-10-750-185-917
; Sequence 917, Application US/10750185
; Publication No. US20050260603A1
; GENERAL INFORMATION:
; APPLICANT: MMI GENOMICS, INC.
; APPLICANT: DENISE, Sue K.
; APPLICANT: KERR, Richard
; APPLICANT: ROSENFELD, David
; APPLICANT: HOLM, Tom
; APPLICANT: BATES, Stephen
; APPLICANT: FANTIN, Dennis
; TITLE OF INVENTION: COMPOSITIONS FOR INFERRING BOVINE TRAITS
; FILE REFERENCE: MM1100-2
; CURRENT APPLICATION NUMBER: US/10750,185
; CURRENT FILING DATE: 2003-12-31
; PRIOR APPLICATION NUMBER: US 60/437,482
; PRIOR FILING DATE: 2002-12-31
; NUMBER OF SEQ ID NOS: 64922
; SOFTWARE: PatentIN version 3.1
; SEQ ID NO 917
; LENGTH: 600
; TYPE: DNA
; ORGANISM: Bovine MMBT02074
US-10-750-185-917

Query Match      17.5%; Score 27.8; DB 6; Length 600;
Best Local Similarity 51.2%; Pred. No. 19;
Matches 65; Conservative 0; Mismatches 62; Indels 0; Gaps 0;

QY 31 GCTATAGAGAGAGCCTCAACCACTTGAATGCTCAACAGCAGCTCAAAAGCTACAGAA 90
Db 250 GGTTTAAAAAGAAATGCTGATATTATTTGTTTAAATGAGAGAAACAAWATAAGAG 309

QY 91 CTATTTATCAATTTCTGCTCATCTTAAATATGCTCTTGTGCTGATCTGTATCATCTGATG 150
Db 310 CTACCCCTCCCTTTTCAGTTTTTTTCTTACTCTTACAAATCTTTGTTACTGTTTGA 369

QY 151 CTCTCTCT 157
Db 370 GTTCTTT 376

RESULT 12
US-10-750-185-60655
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Db	198	CCTTAAATCATGCTATATATTTCCTCCCGATATTTCTCTCCCTG	35
Qy	133	ATCTGTATCATGTCGTCCTC	154
Db	258	GTCTCAATCAGACCATGAGTC	279
RESULT 14			
US-10-750-185-54343/C			
Sequence 54343, Application US/10750185			
Publication No. US20050260603A1			
GENERAL INFORMATION:			
APPLICANT: MMI GENOMICS, INC.			
APPLICANT: DENISE, Sue K.			
APPLICANT: KERR, Richard			
APPLICANT: ROSENFELD, David			
APPLICANT: HOLM, Tom			
APPLICANT: BATES, Stephen			
APPLICANT: FANTIN, Dennis			
TITLE OF INVENTION: COMPOSITIONS FOR INFERRING BOVINE TRAITS			
FILE REFERENCE: MM1100-2			
CURRENT APPLICATION NUMBER: US/10750,185			
CURRENT FILING DATE: 2003-12-31			
PRIOR APPLICATION NUMBER: US 60/437,482			
PRIOR FILING DATE: 2002-12-31			
NUMBER OF SEQ ID NOS: 64922			
SOFTWARE: PatentIN version 3.1			
SEQ ID NO 54343			
LENGTH: 744			
TYPE: DNA			
ORGANISM: Bovine 19866880609777			
US-10-750-185-54343			
Query Match 17.4%; Score 27.6; DB 6; Length 744;			
Best Local Similarity 53.8%; Pred. No. 24;			
Matches 57; Conservative 0; Mismatches 49; Indels 0; Gaps 0			
Qy	52	ATTGAATGCCTCAACAAGCAGTGCTCAAGAAGCTACAGATCTTATCAATTCGTCTC	111
Db	736	AGTGAATCTGAGACCTGCCACCACCAAGGACGAATTTATTTGCAACGTTTGTCTT	677
Qy	112	ATCTTAATATGTCCTTGTCTGATCTGATCATCGTGATGCTTCTCT	157
Db	676	TTCCTTTTGGCTATTGCACACTTGTAATAATTGACATGCTGCT	631
RESULT 15			
US-10-750-185-26340			
Sequence 26340, Application US/10750185			
Publication No. US20050260603A1			
GENERAL INFORMATION:			
APPLICANT: MMI GENOMICS, INC.			
APPLICANT: DENISE, Sue K.			
APPLICANT: KERR, Richard			
APPLICANT: ROSENFELD, David			
APPLICANT: HOLM, Tom			
APPLICANT: BATES, Stephen			
APPLICANT: FANTIN, Dennis			
TITLE OF INVENTION: COMPOSITIONS FOR INFERRING BOVINE TRAITS			
FILE REFERENCE: MM1100-2			
CURRENT APPLICATION NUMBER: US/10750,185			
CURRENT FILING DATE: 2003-12-31			
PRIOR APPLICATION NUMBER: US 60/437,482			
PRIOR FILING DATE: 2002-12-31			
NUMBER OF SEQ ID NOS: 64922			
SOFTWARE: PatentIN version 3.1			
SEQ ID NO 26340			
LENGTH: 1301			
TYPE: DNA			
ORGANISM: Bovine 19866880707421			
US-10-750-185-26340			
Query Match 17.4%; Score 27.6; DB 6; Length 1301;			

Best Local Similarity 53.8%; Pred. No. 29;
Matches 57; Conservative 0; Mismatches 49; Indels 0; Gaps 0;
QY 33 TATAAGAGAGCTCAACCAATTGAATGCCTCAACAGCAGCTCAAAAAGCTACAGAACTCT 92
Db 1177 TAGAATATGCAACTTAAATGATTAAATGGATCAACAAGACATGGCTAGCTACAGATGAA 1236
QY 93 ATTATCAATTTCTGTCTCATCTTAATATGTCTCTTGTCTGATCTGT 138
Db 1237 TGTTCATATGACTATATGCACTCAGATGATATCGCTTATTTAT 1282

RESULT 16
US-10-793-626-1079
; Sequence 1079, Application US/10793626
; Publication No. US20050255478A1
; GENERAL INFORMATION:
; APPLICANT: KIMMERLY, WILLIAM JOHN
; TITLE OF INVENTION: STAPHYLOCOCCUS EPIDERMIDIS NUCLEIC ACIDS AND PROTEINS
; FILE REFERENCE: P03480US
; CURRENT APPLICATION NUMBER: US/10/793,626
; PRIOR FILING DATE: 2004-03-04
; PRIOR APPLICATION NUMBER: 60/164,258
; PRIOR FILING DATE: 1999-11-09
; NUMBER OF SEQ ID NOS: 4472
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 1079
; LENGTH: 1749
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: synthetic
; OTHER INFORMATION: nucleic acid sequence
US-10-793-626-1079

Query Match 17.4%; Score 27.6; DB 6; Length 1749;
Best Local Similarity 60.8%; Pred. No. 32;
Matches 45; Conservative 0; Mismatches 29; Indels 0; Gaps 0;
QY 33 TATAAGAGAGCTCAACCAATTGAATGCCTCAACAGCAGCTCAAAAAGCTACAGAACTCT 92
Db 468 TGTCAAAGAAGATATTACCAATAAATGCCCTAAAGAAGTACCACCAATATATCTCAAGT 527
QY 93 ATTATCAATTTCT 106
Db 528 ATTTAAAGATATTT 541

RESULT 17
US-10-793-626-4436/c
; Sequence 4436, Application US/10793626
; Publication No. US20050255478A1
; GENERAL INFORMATION:
; APPLICANT: KIMMERLY, WILLIAM JOHN
; TITLE OF INVENTION: STAPHYLOCOCCUS EPIDERMIDIS NUCLEIC ACIDS AND PROTEINS
; FILE REFERENCE: P03480US
; CURRENT APPLICATION NUMBER: US/10/793,626
; CURRENT FILING DATE: 2004-03-04
; PRIOR APPLICATION NUMBER: 60/164,258
; PRIOR FILING DATE: 1999-11-09
; NUMBER OF SEQ ID NOS: 4472
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 4436
; LENGTH: 3105
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: synthetic
; OTHER INFORMATION: nucleic acid sequence
US-10-793-626-4436
Query Match 17.4%; Score 27.6; DB 6; Length 3105;
Best Local Similarity 60.8%; Pred. No. 39;

Matches 45; Conservative 0; Mismatches 29; Indels 0; Gaps 0;
QY 33 TATAAGAGAGCTCAACCAATTGAATGCCTCAACAGCAGCTCAAAAAGCTACAGAACTCT 92
Db 669 TGTCAAAGAAGATATTACCAATAAATGCCCTAAAGAAGTACCACCAATATATCTCAAGT 610
QY 93 ATTATCAATTTCT 106
Db 609 ATTTAAAGATATTT 596

RESULT 18
US-10-750-185-51145/c
; Sequence 51145, Application US/10750185
; Publication No. US20050260603A1
; GENERAL INFORMATION:
; APPLICANT: MMI GENOMICS, INC.
; APPLICANT: DENISE, Sue K.
; APPLICANT: KERR, Richard
; APPLICANT: ROSENFELD, David
; APPLICANT: HOLM, Tom
; APPLICANT: BATES, Stephen
; APPLICANT: FANTIN, Dennis
; TITLE OF INVENTION: COMPOSITIONS FOR INFERRING BOVINE TRAITS
; FILE REFERENCE: MM1100-2
; CURRENT APPLICATION NUMBER: US/10/750,185
; CURRENT FILING DATE: 2003-12-31
; PRIOR APPLICATION NUMBER: US 60/437,482
; PRIOR FILING DATE: 2002-12-31
; NUMBER OF SEQ ID NOS: 64922
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 51145
; LENGTH: 1183
; TYPE: DNA
; ORGANISM: Bovine 19866880950653
US-10-750-185-51145

Query Match 17.2%; Score 27.4; DB 6; Length 1183;
Best Local Similarity 52.1%; Pred. No. 32;
Matches 61; Conservative 0; Mismatches 56; Indels 0; Gaps 0;
QY 43 GCCTCAACCAATTGAATGCCTCAACAGCAGCTCAAAAAGCTACAGAACTCTATTATCAAT 102
Db 883 GCCTGTACCATGACTATGACATAACTTACTTAAAAAATGAAATGTTAGTATGTATAAG 824
QY 103 TTCTGTCTCATCTTAATATGTCTTCTGTGATCTGTATCATCTGTATGCTTCTCTGA 159
Db 823 TCCTTTGAGAGTAATAAATCCCTTATAATGACAGCTATTGAGGCTTCTCTGA 767

RESULT 19
US-10-750-185-51810/c
; Sequence 51810, Application US/10750185
; Publication No. US20050260603A1
; GENERAL INFORMATION:
; APPLICANT: MMI GENOMICS, INC.
; APPLICANT: DENISE, Sue K.
; APPLICANT: KERR, Richard
; APPLICANT: ROSENFELD, David
; APPLICANT: HOLM, Tom
; APPLICANT: BATES, Stephen
; APPLICANT: FANTIN, Dennis
; TITLE OF INVENTION: COMPOSITIONS FOR INFERRING BOVINE TRAITS
; FILE REFERENCE: MM1100-2
; CURRENT APPLICATION NUMBER: US/10/750,185
; CURRENT FILING DATE: 2003-12-31
; PRIOR APPLICATION NUMBER: US 60/437,482
; PRIOR FILING DATE: 2002-12-31
; NUMBER OF SEQ ID NOS: 64922
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 51810
; LENGTH: 1305
; TYPE: DNA

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; ORGANISM: Bovine 19866880706323
US-10-750-185-51810

Query Match      17.2%; Score 27.4; DB 6; Length 1305;
Best Local Similarity 50.4%; Pred. No. 33;
Matches 67; Conservative 0; Mismatches 66; Indels 0; Gaps 0;

QY 9 AGTCCAAATACCTCAGTCGCTAGCTATAGAGAGCCTCAACCATGGAAGTCCCTCAACA 68
Db 1093 AATTAATAATCATCACCCTCAGGATAGAGTAGTCTCAACTCTGACAATCAGTGACA 1034
QY 69 AGCAGCTCAAAAGCTACAGATCTATTATCAATTTCTCTCATCTTAATATGCTCTTT 128
Db 1033 GAAATATTAAAGGTCAGAAATGAGTTACAAATATTTCTGTTTGTATTATGATTAT 974
QY 129 GCTGATCTGTATC 141
Db 973 AAAGATGTGACTC 961

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RESULT 20
US-10-750-185-59493/c
; Sequence 59493, Application US/10750185
; Publication No. US20050260603A1
; GENERAL INFORMATION:
; APPLICANT: MMI GENOMICS, INC.
; APPLICANT: DENISE, Sue K.
; APPLICANT: KERR, Richard
; APPLICANT: ROSENFELD, David
; APPLICANT: HOLM, Tom
; APPLICANT: BATES, Stephen
; APPLICANT: FANTIN, Dennis
; TITLE OF INVENTION: COMPOSITIONS FOR INFERRING BOVINE TRAITS
; FILE REFERENCE: MM1100-2
; CURRENT APPLICATION NUMBER: US/10750,185
; CURRENT FILING DATE: 2003-12-31
; PRIOR APPLICATION NUMBER: US 60/437,482
; PRIOR FILING DATE: 2002-12-31
; NUMBER OF SEQ ID NOS: 64922
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 59493
; LENGTH: 2317
; TYPE: DNA
; ORGANISM: Bovine 19866880953651
US-10-750-185-59493

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Query Match      17.2%; Score 27.4; DB 6; Length 2317;
Best Local Similarity 65.6%; Pred. No. 40;
Matches 40; Conservative 0; Mismatches 21; Indels 0; Gaps 0;

QY 96 TATCAATTTCTGCTCATCTTAATATGCTCTGCTGATCTGTATCATGCTGATGCTTCT 155
Db 1027 TATCTTTCTGTTTATACATATTTCTTATGTTTCATGAGCATCATATGTTGATTC 968
QY 156 C 156
Db 967 C 967

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RESULT 21
US-10-750-185-37324
; Sequence 37324, Application US/10750185
; Publication No. US20050260603A1
; GENERAL INFORMATION:
; APPLICANT: MMI GENOMICS, INC.
; APPLICANT: DENISE, Sue K.
; APPLICANT: KERR, Richard
; APPLICANT: ROSENFELD, David
; APPLICANT: HOLM, Tom
; APPLICANT: BATES, Stephen
; APPLICANT: FANTIN, Dennis
; TITLE OF INVENTION: COMPOSITIONS FOR INFERRING BOVINE TRAITS
; FILE REFERENCE: MM1100-2

```

```

; CURRENT APPLICATION NUMBER: US/10750,185
; CURRENT FILING DATE: 2003-12-31
; PRIOR APPLICATION NUMBER: US 60/437,482
; PRIOR FILING DATE: 2002-12-31
; NUMBER OF SEQ ID NOS: 64922
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 37324
; LENGTH: 2563
; TYPE: DNA
; ORGANISM: Bovine 19866880819128
US-10-750-185-37324

Query Match      17.2%; Score 27.4; DB 6; Length 2563;
Best Local Similarity 69.8%; Pred. No. 42;
Matches 37; Conservative 0; Mismatches 16; Indels 0; Gaps 0;

QY 107 GTCTCATCTTAAATATGCTCTTGTCTGATCTCTATCATGCTGATGCTTCTCTGA 159
Db 2307 GTCACCTCTTGAAGTGAGTCTTGTGATCTCTGTAATGATGAGCTGCGTTTA 2359

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RESULT 22
US-11-121-086-81
; Sequence 81, Application US/11121086
; Publication No. US20050266459A1
; GENERAL INFORMATION:
; APPLICANT: POULSEN, TIM S.
; APPLICANT: NIELSEN, KIRSTEN V.
; TITLE OF INVENTION: NUCLEIC ACID PROBES AND NUCLEIC ACID ANALOG PROBES
; FILE REFERENCE: 09138.6000-00000
; CURRENT APPLICATION NUMBER: US/11/121,086
; CURRENT FILING DATE: 2005-05-04
; PRIOR APPLICATION NUMBER: 60/567,570
; PRIOR FILING DATE: 2004-05-04
; NUMBER OF SEQ ID NOS: 107
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 81
; LENGTH: 156544
; TYPE: DNA
; ORGANISM: Homo sapiens
US-11-121-086-81

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```

Query Match      17.2%; Score 27.4; DB 7; Length 156544;
Best Local Similarity 59.7%; Pred. No. 1.6e+02;
Matches 46; Conservative 0; Mismatches 31; Indels 0; Gaps 0;

QY 48 AACCATTTGAAATGCCCTCAACAAGCAGCTCAAAAGCTACAGAACTATTTATCAATTTCTG 107
Db 1093 AACCTTAGAACTAAATAATTCAGTAAAGTTGCCAAATACAGATCAACCTATAAAATCAG 1152
QY 108 TCTCATCTTAAATATGTC 124
Db 1153 TAGCATTCTATATGTC 1169

```

```

RESULT 23
US-11-121-086-97/c
; Sequence 97, Application US/11121086
; Publication No. US20050266459A1
; GENERAL INFORMATION:
; APPLICANT: POULSEN, TIM S.
; APPLICANT: NIELSEN, KIRSTEN V.
; TITLE OF INVENTION: NUCLEIC ACID PROBES AND NUCLEIC ACID ANALOG PROBES
; FILE REFERENCE: 09138.6000-00000
; CURRENT APPLICATION NUMBER: US/11/121,086
; CURRENT FILING DATE: 2005-05-04
; PRIOR APPLICATION NUMBER: 60/567,570
; PRIOR FILING DATE: 2004-05-04
; NUMBER OF SEQ ID NOS: 107
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 97
; LENGTH: 170837
; TYPE: DNA

```

```

; ORGANISM: Homo sapiens
US-11-121-086-97

Query Match      17.2%; Score 27.4; DB 7; Length 170837;
Best Local Similarity 54.5%; Pred. No. 1.7e+02;
Matches 55; Conservative 0; Mismatches 46; Indels 0; Gaps 0;

QY 44 CCTCAACCATTTGAATGCTCAACAGCAGCTCAAAAGCTACAGAAATCTATTATCAATT 103
DB 19319 COTCCACGATTTGTAGGCACTCCCGCCAGCATGTGGAACCTGTATAGTCCAAATAAACCTCTT 19260

QY 104 TCTGTCTCATCTTAATATGTCTCTTGGCTGATCTGATCATC 144
DB 19259 TCTTTGTAATGCCAGTCTCAGGTATGCTTTATCAGC 19219

RESULT 24
US-11-121-086-85
; Sequence 85, Application US/11121086
; Publication No. US20050266459A1
; GENERAL INFORMATION:
; APPLICANT: POULSEN, TIM S.
; APPLICANT: NIELSEN, KIRSTEN V.
; TITLE OF INVENTION: NUCLEIC ACID PROBES AND NUCLEIC ACID ANALOG PROBES
; FILE REFERENCE: 09138.6000-00000
; CURRENT APPLICATION NUMBER: US/11/121,086
; CURRENT FILING DATE: 2005-05-04
; PRIOR APPLICATION NUMBER: 60/567,570
; PRIOR FILING DATE: 2004-05-04
; NUMBER OF SEQ ID NOS: 107
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 85
; LENGTH: 171423
; TYPE: DNA
; ORGANISM: Homo sapiens
US-11-121-086-85

Query Match      17.2%; Score 27.4; DB 7; Length 171423;
Best Local Similarity 53.2%; Pred. No. 1.7e+02;
Matches 58; Conservative 0; Mismatches 51; Indels 0; Gaps 0;

QY 15 ATACCTCACTCGCTCAGCTATAAGAGAGCGCTCAACCAATTAAGTAAATGCTCAACAGCAGC 74
DB 40019 AAAACACGTTTCAAAAAAATAAATAATCTGTAGGACTGATATAACAATCTCTATAAG 40078

QY 75 TCAAAAGCTACAGAAATCTATTATCAATTTCTGTCTCATCTTAATGT 123
DB 40079 TTGTAGTTTACAAATCAACATATCAATATCAATAGTAGCATTCTATATAT 40127

RESULT 25
US-10-793-626-2777/c
; Sequence 2777, Application US/10793626
; Publication No. US20050255478A1
; GENERAL INFORMATION:
; APPLICANT: KIMMERLY, WILLIAM JOHN
; TITLE OF INVENTION: STAPHYLOCOCCUS EPIDERMIDIS NUCLEIC ACIDS AND PROTEINS
; FILE REFERENCE: PU3480US
; CURRENT APPLICATION NUMBER: US/10/793,626
; CURRENT FILING DATE: 2004-03-04
; PRIOR APPLICATION NUMBER: 60/164,258
; PRIOR FILING DATE: 1999-11-09
; NUMBER OF SEQ ID NOS: 4472
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 2777
; LENGTH: 666
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: synthetic
; OTHER INFORMATION: nucleic acid sequence
US-10-793-626-2777
```

```

Query Match      17.1%; Score 27.2; DB 6; Length 666;
Best Local Similarity 64.1%; Pred. No. 30;
Matches 41; Conservative 0; Mismatches 23; Indels 0; Gaps 0;

QY 94 TTTATCAATTTCTCTCATCTTAATATATGCTCTTGTGTGATCTGTATCATCGTGAATGTT 153
DB 540 TTTCTCAAGTCATCTTTTCATATATCAGCCTCTAGATGATCTATAGCATATTGTGCATC 481

QY 154 CTCT 157
DB 480 TTCT 477

RESULT 26
US-10-750-185-52881
; Sequence 52881, Application US/10750185
; Publication No. US20050260603A1
; GENERAL INFORMATION:
; APPLICANT: MMI GENOMICS, INC.
; APPLICANT: DENISE, Sue K.
; APPLICANT: KERR, Richard
; APPLICANT: ROSENFELD, David
; APPLICANT: HOLM, Tom
; APPLICANT: BATES, Stephen
; APPLICANT: FANTIN, Dennis
; TITLE OF INVENTION: COMPOSITIONS FOR INFERRING BOVINE TRAITS
; FILE REFERENCE: MM11100-2
; CURRENT APPLICATION NUMBER: US/10/750,185
; CURRENT FILING DATE: 2003-12-31
; PRIOR APPLICATION NUMBER: US 60/437,482
; PRIOR FILING DATE: 2002-12-31
; NUMBER OF SEQ ID NOS: 64922
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 52881
; LENGTH: 864
; TYPE: DNA
; ORGANISM: Bovine 19866881283242
US-10-750-185-52881

Query Match      17.1%; Score 27.2; DB 6; Length 864;
Best Local Similarity 50.8%; Pred. No. 33;
Matches 65; Conservative 0; Mismatches 63; Indels 0; Gaps 0;

QY 1 ATGGAGAAAGTCCAATPACTCTACTCGCTCAGCTATAAGAGAGCCTCAACCATTTGAAATG 60
DB 373 ATACAAAAAAGCTTCTTTTAAGTAGGCAACCAAAAAACAATAAATGATACAAATGAAAT 432

QY 61 CCTCAACAAGCAGCTCAAAAGCTACAGAAATCTATTATCAATTTCTGTCTCATCTTAATA 120
DB 433 TAAAAAATAAAAAAAGCAAAACCTTCTTAAACAATGAACAAACCCCTGTATTTTCGTATT 492

QY 121 TGTCTCTT 128
DB 493 TTTCTGTT 500

RESULT 27
US-10-793-626-3686
; Sequence 3686, Application US/10793626
; Publication No. US20050255478A1
; GENERAL INFORMATION:
; APPLICANT: KIMMERLY, WILLIAM JOHN
; TITLE OF INVENTION: STAPHYLOCOCCUS EPIDERMIDIS NUCLEIC ACIDS AND PROTEINS
; FILE REFERENCE: PU3480US
; CURRENT APPLICATION NUMBER: US/10/793,626
; CURRENT FILING DATE: 2004-03-04
; PRIOR APPLICATION NUMBER: 60/164,258
; PRIOR FILING DATE: 1999-11-09
; NUMBER OF SEQ ID NOS: 4472
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 3686
; LENGTH: 4136
; TYPE: DNA
```

```

; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: synthetic
; OTHER INFORMATION: nucleic acid sequence
US-10-793-626-3686

Query Match 17.1%; Score 27.2; DB 6; Length 4136;
Best Local Similarity 64.1%; Pred. No. 56;
Matches 41; Conservative 0; Mismatches 23; Indels 0; Gaps 0;

QY 94 TTATCAATTTCTGCTCATCTTAATATGCTCTTGTGATCTGTATCATCGTGATGCTT 153
Db 3518 TTCTCAAGTGCATTTCTTTTCAATCAGCCTCTAGATGATCTATAGCATATTGTGCATC 3577

QY 154 CTCT 157
Db 3578 TTCT 3581

RESULT 28
US-11-121-086-g/c
; Sequence 9, Application US/11121086
; Publication No. US20050266459A1
; GENERAL INFORMATION:
; APPLICANT: POULSEN, TIM S.
; APPLICANT: NIELSEN, KIRSTEN V.
; TITLE OF INVENTION: NUCLEIC ACID PROBES AND NUCLEIC ACID ANALOG PROBES
; FILE REFERENCE: 09138.6000-00000
; CURRENT APPLICATION NUMBER: US/11/121,086
; CURRENT FILING DATE: 2005-05-04
; PRIOR APPLICATION NUMBER: 60/567,570
; PRIOR FILING DATE: 2004-05-04
; NUMBER OF SEQ ID NOS: 107
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 9
; LENGTH: 196200
; TYPE: DNA
; ORGANISM: Homo sapiens
US-11-121-086-g

Query Match 17.1%; Score 27.2; DB 7; Length 196200;
Best Local Similarity 51.7%; Pred. No. 26+02;
Matches 62; Conservative 0; Mismatches 58; Indels 0; Gaps 0;

QY 9 AGTCCAATACCTCACCTCGCTCAGCTATAGAAGAGCCTCAACCAATTGAAATGCCCTCAACA 68
Db 163955 ATTTGAAACCTGAATCTTGGACTTTTCAGTTTGCACAACTCCTTACCTACCCACCA 163899

QY 69 AGCAGCTCAAAAGCTACAGAACTATTATTATCAATTTCTGTCTCATCTTTAAATATGCTCTT 128
Db 163895 CACATATCAACATTTTGTTATATATATATATATATATATATATATATATATATATAT 163983

RESULT 29
US-11-121-086-8/c
; Sequence 8, Application US/11121086
; Publication No. US20050266459A1
; GENERAL INFORMATION:
; APPLICANT: POULSEN, TIM S.
; APPLICANT: NIELSEN, KIRSTEN V.
; TITLE OF INVENTION: NUCLEIC ACID PROBES AND NUCLEIC ACID ANALOG PROBES
; FILE REFERENCE: 09138.6000-00000
; CURRENT APPLICATION NUMBER: US/11/121,086
; CURRENT FILING DATE: 2005-05-04
; PRIOR APPLICATION NUMBER: 60/567,570
; PRIOR FILING DATE: 2004-05-04
; NUMBER OF SEQ ID NOS: 107
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 8
; LENGTH: 246960
; TYPE: DNA
; ORGANISM: Homo sapiens
US-11-121-086-8

```

LOCATION: 230408..230721	
OTHER INFORMATION: exon P complement g34872 gene	
FEATURE:	
NAME/KEY: exon	
LOCATION: 231272..231412	
OTHER INFORMATION: exon Obis complement g34872 gene	
FEATURE:	
NAME/KEY: exon	
LOCATION: 231787..231880	
OTHER INFORMATION: exon O2 complement g34872 gene	
FEATURE:	
NAME/KEY: exon	
LOCATION: 231870..231879	
OTHER INFORMATION: exon O1 complement g34872 gene	
FEATURE:	
NAME/KEY: exon	
LOCATION: 234174..234321	
OTHER INFORMATION: exon O complement g34872 gene	
FEATURE:	
NAME/KEY: exon	
LOCATION: 237406..237428	
OTHER INFORMATION: exon Nbis complement g34872 gene	
FEATURE:	
NAME/KEY: exon	
LOCATION: 239719..239807	
OTHER INFORMATION: exon N2 complement g34872 gene	
FEATURE:	
NAME/KEY: exon	
LOCATION: 239719..239853	
OTHER INFORMATION: exon N complement g34872 gene	
FEATURE:	
NAME/KEY: exon	
LOCATION: 240528..240569	
OTHER INFORMATION: exon M117 complement g34872 gene	
FEATURE:	
NAME/KEY: exon	
LOCATION: 240528..240596	
OTHER INFORMATION: exon M1090 complement g34872 gene	
FEATURE:	
NAME/KEY: exon	
LOCATION: 240528..240617	
OTHER INFORMATION: exon M1069 complement g34872 gene	
FEATURE:	
NAME/KEY: exon	
LOCATION: 240528..240644	
OTHER INFORMATION: exon MS2 complement g34872 gene	
FEATURE:	
NAME/KEY: exon	
LOCATION: 240528..240824	
OTHER INFORMATION: exon M862 complement g34872 gene	
FEATURE:	
NAME/KEY: exon	
LOCATION: 240528..240994	
OTHER INFORMATION: exon M692 complement g34872 gene	
FEATURE:	
NAME/KEY: exon	
LOCATION: 240528..241685	
OTHER INFORMATION: exon M1 complement g34872 gene	
FEATURE:	
NAME/KEY: exon	
LOCATION: 240800..240993	
OTHER INFORMATION: exon MS1 complement g34872 gene	
FEATURE:	
NAME/KEY: misc_feature	
LOCATION: 241686..243685	
OTHER INFORMATION: 5' regulatory region g34872 gene	
FEATURE:	
NAME/KEY: misc_feature	
LOCATION: 290652..292652	
OTHER INFORMATION: 3' regulatory region g34665 gene	
;	
Query Match	17.1%
Best Local Similarity	Score 27.2; DB 7;
	55.2%; Pred. No. 2.2e+02;

Query Match 17.1%; Score 27.2; DB 7; Length 319608;
Best Local Similarity 55.2%; Pred. No. 2.2e+02;

Matches 53; Conservative 0; Mismatches 43; Indels 0; Gaps 0;
QY 23 CTCGCTAGCTATAAGAGAGCCTCAACCAATTGAAATGCTCAACAGCAGCCTCAAAAGC 82
Db 73738 CTAATATCAGTTCTGAAGAGAACTTTCATCTTTAATGCTATATTAGAAATAGCAAA 73679
QY 83 TACAGATCTATTATCAATTTCTCTCACTTAA 118
Db 73678 GTCTAAATACAGTTATCATCTATGCTTTTATCTTAA 73643
RESULT 31
US-10-793-626-2981
; Sequence 2981, Application US/10793626
; Publication No. US20050255478A1
; GENERAL INFORMATION:
; APPLICANT: KIMMERLY, WILLIAM JOHN
; TITLE OF INVENTION: STAPHYLOCOCCUS EPIDERMIDIS NUCLEIC ACIDS AND PROTEINS
; FILE REFERENCE: P03480US
; CURRENT APPLICATION NUMBER: US/10/793,626
; CURRENT FILING DATE: 2004-03-04
; PRIOR APPLICATION NUMBER: 60/164,258
; PRIOR FILING DATE: 1999-11-09
; NUMBER OF SEQ ID NOS: 4472
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 2981
; LENGTH: 742
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURES:
; OTHER INFORMATION: Description of Artificial Sequence: synthetic
; OTHER INFORMATION: nucleic acid sequence
US-10-793-626-2981

Query Match 17.0%; Score 27; DB 6; Length 742;
Best Local Similarity 56.0%; Pred. No. 36;
Matches 51; Conservative 0; Mismatches 40; Indels 0; Gaps 0;
QY 30 AGCTATAAGAGAGCCTCAACCAATTGAAATGCTCAACAGCAGCCTCAAAAGCTACAGAA 89
Db 556 AGATAAAGGAATGAGTAAGATTAGATTTCATATTAGTACATCAGAGCCTAAAAAA 615
QY 90 TCATTATCAATTTCTGCTCATCTTAATA 120
Db 616 GTTCAACAACAATTTCTCGTATTCCGAATA 646

RESULT 32
US-10-750-185-36690
; Sequence 36690, Application US/10750185
; Publication No. US20050260603A1
; GENERAL INFORMATION:
; APPLICANT: MMI GENOMICS, INC.
; APPLICANT: DENISE, Sue K.
; APPLICANT: KERR, Richard
; APPLICANT: ROSENFELD, David
; APPLICANT: HOLM, Tom
; APPLICANT: BATES, Stephen
; APPLICANT: FANTIN, Dennis
; TITLE OF INVENTION: COMPOSITIONS FOR INFERRING BOVINE TRAITS
; FILE REFERENCE: MM1100-2
; CURRENT APPLICATION NUMBER: US/10/750,185
; CURRENT FILING DATE: 2003-12-31
; PRIOR APPLICATION NUMBER: US 60/437,482
; PRIOR FILING DATE: 2002-12-31
; NUMBER OF SEQ ID NOS: 64922
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 36690
; LENGTH: 2116
; TYPE: DNA
; ORGANISM: Bovine 1986680917915
US-10-750-185-36690

Query Match 17.0%; Score 27; DB 6; Length 2116;
Best Local Similarity 60.0%; Pred. No. 51;
Matches 45; Conservative 0; Mismatches 30; Indels 0; Gaps 0;
QY 5 AGAAAGTCCAATACCTCACTCGCTCAGCTATAAGAGAGCCTCAACCAATTGAAATGCTC 64
Db 707 AAAAATCCAAATTCGCCCAAAATTCAGCTATAATTTGAACAGCCCAACAGACGCCAA 766
QY 65 AACAGAGCAGTCAAA 79
Db 767 AACAAATCATGAAAAA 781

RESULT 33
US-10-750-185-57047/c
; Sequence 57047, Application US/10750185
; Publication No. US20050260603A1
; GENERAL INFORMATION:
; APPLICANT: MMI GENOMICS, INC.
; APPLICANT: DENISE, Sue K.
; APPLICANT: KERR, Richard
; APPLICANT: ROSENFELD, David
; APPLICANT: HOLM, Tom
; APPLICANT: BATES, Stephen
; APPLICANT: FANTIN, Dennis
; TITLE OF INVENTION: COMPOSITIONS FOR INFERRING BOVINE TRAITS
; FILE REFERENCE: MM1100-2
; CURRENT APPLICATION NUMBER: US/10/750,185
; CURRENT FILING DATE: 2003-12-31
; PRIOR APPLICATION NUMBER: US 60/437,482
; PRIOR FILING DATE: 2002-12-31
; NUMBER OF SEQ ID NOS: 64922
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 57047
; LENGTH: 2332
; TYPE: DNA
; ORGANISM: Bovine 1986680788543
US-10-750-185-57047

Query Match 17.0%; Score 27; DB 6; Length 2332;
Best Local Similarity 51.2%; Pred. No. 53;
Matches 63; Conservative 0; Mismatches 60; Indels 0; Gaps 0;
QY 33 TATAAGAGAGCCTCAACCAATTGAAATGCTCAACAGCAGCCTCAAAAGCTACAGAACT 92
Db 1575 TGTAAATGAAACCAACAATCAAGGGGCTTAAGGATCATGCGTGCATCTCCCTTAGCA 1516
QY 93 ATTATCAATTTCTGCTCATCTTAATATGCTCTTGTGATCTGTATCATCTGATGCT 152
Db 1515 ACTAGTTTCTAGTGTGTCAGTTAGATTACTATTAAATGTTGAATTAATTTATTTGAT 1456
QY 153 TCT 155
Db 1455 TTT 1453

RESULT 34
US-10-750-185-30659/c
; Sequence 30659, Application US/10750185
; Publication No. US20050260603A1
; GENERAL INFORMATION:
; APPLICANT: MMI GENOMICS, INC.
; APPLICANT: DENISE, Sue K.
; APPLICANT: KERR, Richard
; APPLICANT: ROSENFELD, David
; APPLICANT: HOLM, Tom
; APPLICANT: BATES, Stephen
; APPLICANT: FANTIN, Dennis
; TITLE OF INVENTION: COMPOSITIONS FOR INFERRING BOVINE TRAITS
; FILE REFERENCE: MM1100-2
; CURRENT APPLICATION NUMBER: US/10/750,185
; CURRENT FILING DATE: 2003-12-31
; PRIOR APPLICATION NUMBER: US 60/437,482

```

; PRIOR FILING DATE: 2002-12-31
; NUMBER OF SEQ ID NOS: 64922
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 30659
; LENGTH: 2744
; TYPE: DNA
; ORGANISM: Bovine 19866880683089
US-10-750-185-30659

Query Match 17.0%; Score 27; DB 6; Length 2744;
Best Local Similarity 56.0%; Pred.No. 56;
Matches 51; Conservative 0; Mismatches 40; Indels 0; Gaps 0;

QY 49 ACCATTGAAATGCCCTCAACAGCAGCGTCAAAGCTACAGAATCTATTATCAATTTCTGT 108
||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 2513 ACGACTGAAGCGACTTAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAG 2454
||||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||

QY 109 CTCATCTTAATATGTCCTTGCTGCATCTGTA 139
||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 2453 TTTTCTCTCTATATAGTTATTATTGGGA 2423
||||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||

RESULT 35
US-10-793-626-3660
; Sequence 3660, Application US/10793626
; Publication No. US20050255478A1
; GENERAL INFORMATION:
; APPLICANT: KIMMERLY, WILLIAM JOHN
; TITLE OF INVENTION: STAPHYLOCOCCUS EPIDERMIDIS NUCLEIC ACIDS AND PROTEINS
; FILE REFERENCE: PU3480US
; CURRENT APPLICATION NUMBER: US/10/793,626
; CURRENT FILING DATE: 2004-03-04
; PRIOR APPLICATION NUMBER: 60/164,258
; PRIOR FILING DATE: 1999-11-09
; NUMBER OF SEQ ID NOS: 4472
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 3660
; LENGTH: 3048
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: synthetic
; OTHER INFORMATION: nucleic acid sequence
US-10-793-626-3660

Query Match 17.0%; Score 27; DB 6; Length 3048;
Best Local Similarity 56.0%; Pred.No. 58;
Matches 51; Conservative 0; Mismatches 40; Indels 0; Gaps 0;

QY 30 AGCTATAAGAGAGCGCTCAACCATTGAAATGCCCTCAACAGCAGCGTCAAAGCTACAGAA 89
||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 1128 AGATATAAGGAATGAGTAAGATTTAGATTTCATATTAGTACATCAGAGCGCTAAAAA 1187
||||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||

QY 90 TCTATTATCAATTTCTGCTCATCTTAATA 120
||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 1188 GTTCAACAACAATTACTTCGTATTCCGAATA 1218
||||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||

RESULT 36
US-10-793-626-3889
; Sequence 3889, Application US/10793626
; Publication No. US20050255478A1
; GENERAL INFORMATION:
; APPLICANT: KIMMERLY, WILLIAM JOHN
; TITLE OF INVENTION: STAPHYLOCOCCUS EPIDERMIDIS NUCLEIC ACIDS AND PROTEINS
; FILE REFERENCE: PU3480US
; CURRENT APPLICATION NUMBER: US/10/793,626
; CURRENT FILING DATE: 2004-03-04
; PRIOR APPLICATION NUMBER: 60/164,258
; PRIOR FILING DATE: 1999-11-09
; NUMBER OF SEQ ID NOS: 4472
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 3889

```

```

; LENGTH: 4113
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-624-932-21

Query Match
Best Local Similarity 17.0%; Score 27; DB 6; Length 4113;
Matches 69; Conservative 0; Mismatches 70; Indels 0; Gaps 0;

QY 20 TCACCTCGCTAGCTATAGAGAGCCCTCAACCATTTGAAATGCTCAACAGCAGCTCAAA 79
DB 3934 TAACAATCCTAGCTTTTAAAGAAACTATTAAATGTAATAATTTCTACATGTCATTCAGA 3993
QY 80 AGCTACAGAAATCTATTATCAATTTCTGCTCATCTTAATATGCTCTTCTGCTGATCTGTA 139
DB 3994 TATTATGATATCTTCTAGCCTTTATCTGACTTTTAAATGTACATATTTCTGCTTGGC 4053
QY 140 TCATCGTGAATCTCTCTG 158
DB 4054 TGATTGTATATTTCACTG 4072

RESULT 38
US-11-108-528-27
; Sequence 27, Application US/11108528
; Publication No. US20050261189A1
; GENERAL INFORMATION:
; APPLICANT: Larsen, Glenn
; APPLICANT: Marvin, Martha
; APPLICANT: Li, Dean Y.
; APPLICANT: Wang, Elizabeth
; APPLICANT: Chen, C. M. Amy
; APPLICANT: Shamah, Steven M.
; TITLE OF INVENTION: METHODS OF PROMOTING CARDIAC CELL
; FILE REFERENCE: HYDR-P01-041
; CURRENT APPLICATION NUMBER: US/11/108,528
; CURRENT FILING DATE: 2005-04-18
; PRIOR APPLICATION NUMBER: US 60/563,137
; PRIOR FILING DATE: 2004-04-16
; PRIOR APPLICATION NUMBER: US 60/598,368
; PRIOR FILING DATE: 2004-08-02
; NUMBER OF SEQ ID NOS: 86
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 27
; LENGTH: 5855
; TYPE: DNA
; ORGANISM: Homo sapiens
US-11-108-528-27

Query Match
Best Local Similarity 17.0%; Score 27; DB 7; Length 5855;
Matches 69; Conservative 0; Mismatches 70; Indels 0; Gaps 0;

QY 20 TCACCTCGCTAGCTATAGAGAGCCCTCAACCATTTGAAATGCTCAACAGCAGCTCAAA 79
DB 3759 TAACAATCCTAGCTTTTAAAGAAACTATTAAATGTAATAATTTCTACATGTCATTCAGA 3818
QY 80 AGCTACAGAAATCTATTATCAATTTCTGCTCATCTTTAAATGCTCTTCTGCTGATCTGTA 139
DB 3819 TATTATGATATCTTCTAGCCTTTATCTGACTTTTAAATGTACATATTTCTGCTTGGC 3878
QY 140 TCATCGTGAATCTCTCTG 158
DB 3879 TGATTGTATATTTCACTG 3897

RESULT 39
US-11-112-908-19
; Sequence 19, Application US/11112908
; Publication No. US20050260659A1
; GENERAL INFORMATION:
; APPLICANT: Harris, Cole

```

Db	114	AACCTTGGAATATGCTGTTTAATGTTCAATG	81
RESULT 41			
US-10-750-185-55086			
; Sequence 55086, Application US/10750185			
; Publication No. US20050260603A1			
; GENERAL INFORMATION:			
; APPLICANT: MMI GENOMICS, INC.			
; APPLICANT: DENISE, Sue K.			
; APPLICANT: KERR, Richard			
; APPLICANT: ROSENFELD, David			
; APPLICANT: HOLM, Tom			
; APPLICANT: BATES, Stephen			
; APPLICANT: FANTIN, Dennis			
; TITLE OF INVENTION: COMPOSITIONS FOR INFERRING BOVINE TRAITS			
; FILE REFERENCE: MM1100-2			
; CURRENT FILING DATE: 2003-12-31			
; PRIOR APPLICATION NUMBER: US 60/437,482			
; PRIOR FILING DATE: 2002-12-31			
; NUMBER OF SEQ ID NOS: 64922			
; SOFTWARE: PatentIN version 3.1			
; SEQ ID NO 55086			
; LENGTH: 1320			
; TYPE: DNA			
; ORGANISM: Bovine 19866880846515			
US-10-750-185-55086			
Query Match 16.9%; Score 26.8; DB 6; Length 1320;			
Best Local Similarity 57.0%; Pred. No. 50;			
Matches 49; Conservative 0; Mismatches 37; Indels 0; Gaps 0;			
Qy	74	GTCAAAGCTACAGAACTCTATTATCAATTTCTGTCTCACTTAATATCTCTCTGCTGA	133
Db	699	GTAACATGCTATACAATGATGTTACAATGTAATATCTATTATCATTTATTTGTTCT	758
Qy	134	TCGTATCATCGTGAGCTTCTCTGA	159
Db	759	TATGAGAATTATGTGCGCATGACTTA	784
RESULT 42			
US-10-750-185-33223			
; Sequence 33223, Application US/10750185			
; Publication No. US20050260603A1			
; GENERAL INFORMATION:			
; APPLICANT: MMI GENOMICS, INC.			
; APPLICANT: DENISE, Sue K.			
; APPLICANT: KERR, Richard			
; APPLICANT: ROSENFELD, David			
; APPLICANT: HOLM, Tom			
; APPLICANT: BATES, Stephen			
; APPLICANT: FANTIN, Dennis			
; TITLE OF INVENTION: COMPOSITIONS FOR INFERRING BOVINE TRAITS			
; FILE REFERENCE: MM1100-2			
; CURRENT APPLICATION NUMBER: US/10750,185			
; CURRENT FILING DATE: 2003-12-31			
; PRIOR APPLICATION NUMBER: US 60/437,482			
; PRIOR FILING DATE: 2002-12-31			
; NUMBER OF SEQ ID NOS: 64922			
; SOFTWARE: PatentIN version 3.1			
; SEQ ID NO 33223			
; LENGTH: 1733			
; TYPE: DNA			
; ORGANISM: Bovine 19866880464123			
US-10-750-185-33223			
Query Match 16.9%; Score 26.8; DB 6; Length 1733;			
Best Local Similarity 49.3%; Pred. No. 55;			
Matches 70; Conservative 0; Mismatches 72; Indels 0; Gaps 0;			
Qy	12	CCATACCTCACTCGCTCAGCTATAAGAGAGCCTCAACCAATTCGAAATGCTCAACAAGC	71
Db	1054	CAAACTACCTCATATCTTACATATATGAGGTGTTCCAGGAAAAATGAAAAACAAGAAAT	1113
Qy	72	ACGTCAAAAGCTACAGAAATCTATTATTAATTTCTGTCTCAATCTTAATATATCTCTTGCT	131
Db	1114	AAACCAAAACAAAAAAGAAAAAAGAACTGTTCCAGCAGACAGAAAGATGGGTTCCG	1173
Qy	132	GATCTGATCATCGTGATGCTT	153
Db	1174	GAATTTCTAATTCAGTTGGTT	1195
RESULT 43			
US-10-131-826A-409/c			
; Sequence 409, Application US/10131826A			
; Publication No. US20050245730A1			
; GENERAL INFORMATION:			
; APPLICANT: Baker, Kevin P.			
; APPLICANT: Beresini, Maureen			
; APPLICANT: DeForge, Laura			
; APPLICANT: Desnoyers, Luc			
; APPLICANT: Filvaroff, Ellen			
; APPLICANT: Gao, Wei-Qiang			
; APPLICANT: Gerritsen, Mary E.			
; APPLICANT: Goddard, Audrey			
; APPLICANT: Godowski, Paul J.			
; APPLICANT: Gurney, Austin L.			
; APPLICANT: Sherwood, Steven			
; APPLICANT: Smith, Victoria			
; APPLICANT: Stewart, Timothy A.			
; APPLICANT: Tumas, Daniel			
; APPLICANT: Watanabe, Colin K			
; APPLICANT: Wood, William			
; APPLICANT: Zhang, Zemin			
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC			
; FILE REFERENCE: P3330R1C128			
; CURRENT APPLICATION NUMBER: US/10/131,826A			
; CURRENT FILING DATE: 2002-04-24			
; PRIOR APPLICATION NUMBER: 60/049911			
; PRIOR FILING DATE: 1997-06-18			
; PRIOR APPLICATION NUMBER: 60/056974			
; PRIOR FILING DATE: 1997-08-26			
; PRIOR APPLICATION NUMBER: 60/059113			
; PRIOR FILING DATE: 1997-09-17			
; PRIOR APPLICATION NUMBER: 60/059115			
; PRIOR FILING DATE: 1997-09-17			
; PRIOR APPLICATION NUMBER: 60/059117			
; PRIOR FILING DATE: 1997-09-17			
; PRIOR APPLICATION NUMBER: 60/059122			
; PRIOR FILING DATE: 1997-09-17			
; PRIOR APPLICATION NUMBER: 60/059184			
; PRIOR FILING DATE: 1997-09-17			
; PRIOR APPLICATION NUMBER: 60/059263			
; PRIOR FILING DATE: 1997-09-18			
; PRIOR APPLICATION NUMBER: 60/059352			
; PRIOR FILING DATE: 1997-09-19			
; PRIOR APPLICATION NUMBER: 60/059588			
; PRIOR FILING DATE: 1997-09-19			
; Remaining Prior Application data removed - See File Wrapper or PALM.			
; NUMBER OF SEQ ID NOS: 550			
; SEQ ID NO 409			
; LENGTH: 3617			
; TYPE: DNA			
; ORGANISM: Homo Sapien			
US-10-131-826A-409			
Query Match 16.9%; Score 26.8; DB 6; Length 3617;			
Best Local Similarity 55.3%; Pred. No. 71;			
Matches 52; Conservative 0; Mismatches 42; Indels 0; Gaps 0;			
Qy	63	TCAACAAGCAGCTCAAAAGCTACAGAAATCTATTATCAATTTCTGTCTCATCTTAATATG	122

Accession	Gene	Strain	Accession	Gene	Strain
62237	db	AACTATAAGG	62237	db	AACTATAAGG
90	Qy	TCAATTATCA	90	Qy	TCAATTATCA
62297	Db	TCAATTATCA	62297	Db	TCAATTATCA

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RESULT 46
US-11-121-086-96/c
; Sequence 96, Application US/11121086
; Publication No. US20050266459A1
; GENERAL INFORMATION:
; APPLICANT: POULSEN, TIM S.
; APPLICANT: NIELSEN, KIRSTEN V.
; TITLE OF INVENTION: NUCLEIC ACID PROBES AND NUCLEIC ACID ANALOG PROBES
; FILE REFERENCE: 09138.6000-00000
; CURRENT APPLICATION NUMBER: US/11/121,086
; CURRENT FILING DATE: 2005-05-04
; PRIOR APPLICATION NUMBER: 60/567,570
; PRIOR FILING DATE: 2004-05-04
; NUMBER OF SEQ ID NOS: 107
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 96
; LENGTH: 139054
; TYPE: DNA
; ORGANISM: Homo sapiens
US-11-121-086-96

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	Query Match	16.9%	Score 26.8;	DB 7;	Length 139054;
	Best Local Similarity	55.3%	Pred. No. 2.3e+02;		
	Matches	52;	Conservative 0;	Mismatches 42;	Indels 0; Gaps 0;
QY	44	CCTCAACATTGAAATGGCTCAACAGCACGTCACAAAGCTACAGAATCTATTTATCAATT	103		
Db	52932	CGTGAATCTCTAGATGAAGCAACAAATTGAGTAAATCTTACAGAATCCAATCATCTAGG			
QY	104	TCTGTCTCATTTAATATGCTCTTGTGATCTG	137		
Db	52872	GCTGACCCATCATATAATTGAAATGGCTATGTG	52839		

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RESULT 47
US-11-121-086-93
; Sequence 93, Application US/11121086
; Publication No. US20050266459A1
; GENERAL INFORMATION:
; APPLICANT: POULSEN, TIM S.
; APPLICANT: NIELSEN, KIRSTEN V.
; TITLE OF INVENTION: NUCLEIC ACID PROBES AND NUCLEIC ACID ANALOG PROBES
; FILE REFERENCE: 09138.6000-00000
; CURRENT APPLICATION NUMBER: US/11/121,086
; CURRENT FILING DATE: 2005-05-04
; PRIOR APPLICATION NUMBER: 60/567,570
; PRIOR FILING DATE: 2004-05-04
; NUMBER OF SEQ ID NOS: 107
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 93
; LENGTH: 156735
; TYPE: DNA
; ORGANISM: Homo sapiens
US-11-121-086-93

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Query Match	16.9%	Score 26.8;	DB 7;	Length 156735;
Best Local Similarity	52.7%;	Pred. No. 2.4e+02;		
Matches 58;	Conservative 0;	Mismatches 0;	Indels 0;	Gaps 0;
31	GCTATAAGAGAGCCTCAACATTGAAATGCCCTCAACAGACGCTCAAAGCTACAGAAAT	90		
77555	GCCAAAGACAAATCATCAGCACACCCAGCTATGCACAGAAATGGAAGCAGGGAAT	77614		
91	CTATTTATCAATTTCTGTCTCATCTTAAATATGCTCTCTTGTCTGATCTGAT	140		

Db	77615	AAATTTATATTTCTGTCAAATTGTTACATGAAATTTATTTATATAT	77664
RESULT 48			
US-10-750-185-32215/c			
; Sequence 32215, Application US/10750185			
; Publication No. US20050260603A1			
; GENERAL INFORMATION:			
; APPLICANT: MMI GENOMICS, INC.			
; APPLICANT: DENISE, Sue K.			
; APPLICANT: KERR, Richard			
; APPLICANT: ROSENFELD, David			
; APPLICANT: HOLM, Tom			
; APPLICANT: BATES, Stephen			
; APPLICANT: FANTIN, Dennis			
; TITLE OF INVENTION: COMPOSITIONS FOR INFERRING BOVINE TRAITS			
; FILE REFERENCE: MM11100-2			
; CURRENT APPLICATION NUMBER: US/10/750,185			
; CURRENT FILING DATE: 2003-12-31			
; PRIOR APPLICATION NUMBER: US 60/437,482			
; PRIOR FILING DATE: 2002-12-31			
; NUMBER OF SEQ ID NOS: 64922			
; SOFTWARE: PatentIn version 3.1			
; SEQ ID NO 32215			
; LENGTH: 847			
; TYPE: DNA			
; ORGANISM: Bovine 19866881406535			
US-10-750-185-32215			
Query Match 16.7%; Score 26.6; DB 6; Length 847;			
Best Local Similarity 63.1%; Pred. No. 49;			
Matches 41; Conservative 0; Mismatches 24; Indels 0; Gaps 0;			
Qy	28	TCAGCTATAGAGAGCCTCAACCAATTGAATGCCCTCAACAGCAGCTCAAAAGCTACAG	87
Db	211	TCAGATATATACAGCTGCTAAATTCATGAGTGACTCTATCAACATTTATCAAGATACAG	152
Qy	88	AATCT 92	
Db	151	AAGCT 147	
RESULT 49			
US-11-112-908-135/c			
; Sequence 135, Application US/11112908			
; Publication No. US20050260659A1			
; GENERAL INFORMATION:			
; APPLICANT: Harris, Cole			
; APPLICANT: Davis, Lisa M.			
; TITLE OF INVENTION: Breast Cancer Biomarkers			
; FILE REFERENCE: 04-164-US			
; CURRENT APPLICATION NUMBER: US/11/112,908			
; CURRENT FILING DATE: 2005-04-22			
; PRIOR APPLICATION NUMBER: US 60/564,758			
; PRIOR FILING DATE: 2004-04-23			
; PRIOR APPLICATION NUMBER: US 60/575,978			
; PRIOR FILING DATE: 2004-06-01			
; PRIOR APPLICATION NUMBER: US 60/631,702			
; PRIOR FILING DATE: 2004-11-30			
; PRIOR APPLICATION NUMBER: US 60/633,826			
; PRIOR FILING DATE: 2004-12-07			
; NUMBER OF SEQ ID NOS: 511			
; SOFTWARE: PatentIn version 3.3			
; SEQ ID NO 135			
; LENGTH: 1197			
; TYPE: DNA			
; ORGANISM: Homo sapiens			
US-11-112-908-135			
Query Match 16.7%; Score 26.6; DB 7; Length 1197;			
Best Local Similarity 58.0%; Pred. No. 55;			
Matches 47; Conservative 0; Mismatches 34; Indels 0; Gaps 0;			
Qy	77	AAAAGCTACAGAACTCTATTTATCAATTTCTGCTCATCTTAATATATCTCTTCTGCTGATCT	136
Db	583	AAAAGTTACATGATTGATGGGAAATTTTATTCTCATCATATTAAGTATTTTAAATACAT	524
Qy	137	GTATCATCGTGATGCTTCTCT	157
Db	523	TGTAAACCTGGAGATATTTCT	503
RESULT 50			
US-10-750-185-30040			
; Sequence 30040, Application US/10750185			
; Publication No. US20050260603A1			
; GENERAL INFORMATION:			
; APPLICANT: MMI GENOMICS, INC.			
; APPLICANT: DENISE, Sue K.			
; APPLICANT: KERR, Richard			
; APPLICANT: ROSENFELD, David			
; APPLICANT: HOLM, Tom			
; APPLICANT: BATES, Stephen			
; APPLICANT: FANTIN, Dennis			
; TITLE OF INVENTION: COMPOSITIONS FOR INFERRING BOVINE TRAITS			
; FILE REFERENCE: MM11100-2			
; CURRENT APPLICATION NUMBER: US/10/750,185			
; CURRENT FILING DATE: 2003-12-31			
; PRIOR APPLICATION NUMBER: US 60/437,482			
; PRIOR FILING DATE: 2002-12-31			
; NUMBER OF SEQ ID NOS: 64922			
; SOFTWARE: PatentIn version 3.1			
; SEQ ID NO 30040			
; LENGTH: 1256			
; TYPE: DNA			
; ORGANISM: Bovine 19866881910681			
US-10-750-185-30040			
Query Match 16.7%; Score 26.6; DB 6; Length 1256;			
Best Local Similarity 48.4%; Pred. No. 56;			
Matches 74; Conservative 0; Mismatches 79; Indels 0; Gaps 0;			
Qy	5	AGAAAGTCCAATACCTCACTCGCTCAGCTATAGAAGAGCCTCAACCAATTGAAATGCCCTC	64
Db	278	AGAAGGGACAAGTCATAGGTTTATTTAAATAGGAGATCTCTAATGACTTGTTCCTT	337
Qy	65	AACAAGCAGCTCAAAAAGCTACAGAAATCTATTATTCATATTTCTGCTCATCTTTAATATGTC	124
Db	338	CACAGTTAACTTTTAAGAAACCATGTTATTTTATTTATATTTGTATATTATTGCACTGT	397
Qy	125	TCTTGCTGATCTGTATCATCGTGATGCTTCTCT	157
Db	398	TTTCACTGTTTCAGTTTTAAATACAAAGCTGATCT	430
Search completed: December 8, 2005, 04:35:44			
Job time : 654 secs			

GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: December 7, 2005, 23:56:51 ; Search time 3746 Seconds
(without alignments)
1985.891 Million cell updates/sec

Title: US-10-691-412-1

Perfect score: 159

Sequence: 1 atgagaaagtccaataacct.....tcacgtgatgcttctctga 159

Scoring table: IDENTITY NUC

Gapop 10.0 , Gapext 1.0

Searched: 41078325 seqs, 23393541228 residues

Total number of hits satisfying chosen parameters: 82156650

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 100 summaries

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1: gb_est1.*

2: gb_est2.*

3: gb_est3.*

4: gb_est4.*

5: gb_est5.*

6: gb_est6.*

7: gb_est7.*

8: gb_est8.*

9: gb_gsa1.*

10: gb_gsa2.*

11: gb_gsa3.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
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2	159	100.0	376	5	C05636
3	159	100.0	383	1	AL599452
4	159	100.0	408	1	AL600669
5	159	100.0	412	1	AL601169
6	159	100.0	412	5	C04012
7	159	100.0	426	1	AJ710051
8	159	100.0	426	7	CN411469
9	159	100.0	431	1	AL601173
10	159	100.0	433	1	AL600088
11	159	100.0	438	5	C02888
12	159	100.0	443	1	AI190578
13	159	100.0	448	5	C03252
14	159	100.0	451	5	C04050
15	159	100.0	455	1	AL601166
16	159	100.0	477	1	AL599208
17	159	100.0	478	1	AL600135
18	159	100.0	479	1	AL601279
19	159	100.0	482	1	AL601190
20	159	100.0	533	1	AJ708798
21	159	100.0	533	5	C03682
22	159	100.0	534	1	AJ709272

23	159	100.0	540	1	AL600427
24	159	100.0	541	1	AJ712160
25	159	100.0	543	1	AL600196
26	159	100.0	547	1	AL600489
27	159	100.0	548	1	AJ708988
28	159	100.0	550	3	BP257178
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31	159	100.0	550	3	BP260039
32	159	100.0	551	3	BP260274
33	159	100.0	551	3	BP259171
34	159	100.0	551	3	BP259965
35	159	100.0	552	1	AL600429
36	159	100.0	552	3	BP259458
37	159	100.0	553	3	BP257543
38	159	100.0	554	3	BP258625
39	159	100.0	556	3	BP257310
40	159	100.0	558	3	BP258394
41	159	100.0	558	3	BP258989
42	159	100.0	559	1	AI720214
43	159	100.0	559	3	BP260265
44	159	100.0	560	3	BP257291
45	159	100.0	561	1	AL600477
46	159	100.0	561	3	BP257982
47	159	100.0	562	3	BP258939
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49	159	100.0	563	3	BP258507
50	159	100.0	563	3	BP257372
51	159	100.0	563	3	BP257855
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55	159	100.0	564	3	BP258958
56	159	100.0	564	3	BP259773
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60	159	100.0	566	1	AL600027
61	159	100.0	566	3	BP259059
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65	159	100.0	567	3	BP260314
66	159	100.0	568	3	BP257983
67	159	100.0	568	3	BP258837
68	159	100.0	568	3	BP259285
69	159	100.0	569	3	BP257604
70	159	100.0	569	3	BP258334
71	159	100.0	569	3	BP258723
72	159	100.0	569	3	BP259517
73	159	100.0	570	3	BP259093
74	159	100.0	571	3	BP257806
75	159	100.0	571	3	BP258451
76	159	100.0	571	3	BP258954
77	159	100.0	572	3	BP257207
78	159	100.0	572	3	BP260018
79	159	100.0	573	3	BP258250
80	159	100.0	573	3	BP260038
81	159	100.0	575	3	BP213150
82	159	100.0	575	3	BP259468
83	159	100.0	576	3	BP258116
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85	159	100.0	577	3	BP277592
86	159	100.0	578	3	BP257169
87	159	100.0	578	3	BP257607
88	159	100.0	578	3	BP257631
89	159	100.0	578	3	BP259492
90	159	100.0	579	3	BP257557
91	159	100.0	579	3	BP258523
92	159	100.0	579	3	BP258972
93	159	100.0	579	3	BP259815
94	159	100.0	580	1	AJ310795
95	159	100.0	580	3	BP257104

96	159	100.0	580	3	BP257141	BP257141
97	159	100.0	580	3	BP257154	BP257154
98	159	100.0	580	3	BP257167	BP257167
99	159	100.0	580	3	BP257171	BP257171
100	159	100.0	580	3	BP257191	BP257191
ALIGNMENTS						
RESULT 1	159 bp DNA linear GSS 02-JUN-2005					
LOCUS	DQ046231 Homo sapiens PLN gene, VIRTUAL TRANSCRIPT, partial sequence, genomic survey sequence.					
DEFINITION	DQ046231					
ACCESSION	DQ046231.1 GI:66897446					
VERSION	GSS.					
KEYWORDS	Homo sapiens (human)					
SOURCE	Homo sapiens					
ORGANISM	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae; Homo.					
REFERENCE	1 (bases 1 to 159)					
AUTHORS	Nielsen,R., Bustamante,C., Clark,A.G., Glanowski,S., Sackton,T.B., Hubisz,M.J., Fiedel-Alon,A., Tanenbaum,D.M., Cividello,D., White,T.J., Sninsky,J.J., Adams,M.D. and Cargill,M.					
TITLE	A Scan for Positively Selected Genes in the Genomes of Humans and Chimpanzees					
JOURNAL	(er) PLoS Biol. 3 (6), E170 (2005)					
PUBMED	15869325					
REFERENCE	2 (bases 1 to 159)					
AUTHORS	Nielsen,R., Bustamante,C., Clark,A.G., Glanowski,S., Sackton,T.B., Hubisz,M.J., Fiedel-Alon,A., Tanenbaum,D.M., Cividello,D., White,T.J., Sninsky,J.J., Adams,M.D. and Cargill,M.					
TITLE	Direct Submission					
JOURNAL	Submitted (05-MAY-2005) Celera Genomics, 45 West Gude Drive, Rockville, MD 20850, USA					
COMMENT	This sequence was made by sequencing genomic exons and ordering them based on alignment. Translation starts at the beginning of alignment.					
FEATURES	Location/Qualifiers					
source	1..159 /organism="Homo sapiens" /mol_type="genomic DNA" /db_xref="taxon:9606" /chromosome="6" <1..>159 /gene="PLN" /locus_tag="HC12009"					
gene						
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QY	1 ATGAGAGAAAGTCCAATACCTCCTCGCTCAGCTATAGAAGAGCGCTCAACATTGAAATG 60					
DB	1 ATGAGAGAAAGTCCAATACCTCCTCGCTCAGCTATAGAAGAGCGCTCAACATTGAAATG 60					
QY	61 CCTCAACAGCAGCTCAAAAGCTACAGAACTATTATCAATTTCTGCTCATCTTAATA 120					
DB	61 CCTCAACAGCAGCTCAAAAGCTACAGAACTATTATCAATTTCTGCTCATCTTAATA 120					
QY	121 TGTCTCTTGTGATCTGTATCATCGTATGCTTCTCTGA 159					
DB	121 TGTCTCTTGTGATCTGTATCATCGTATGCTTCTCTGA 159					
RESULT 2	376 bp mRNA linear EST 30-JUL-1996					
LOCUS	C05636 Human heart cDNA (Ynakamura) Homo sapiens cDNA clone					
DEFINITION	C05636					

3NHC5059, mRNA sequence.	3NHC5059, mRNA sequence.
C05636	C05636
VERSION	GI:1468887
KEYWORDS	EST.
SOURCE	Homo sapiens (human)
ORGANISM	Homo sapiens
	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae; Homo.
REFERENCE	1 (bases 1 to 376)
AUTHORS	Tanaka,T., Ogiwara,A., Uchiyama,I., Takagi,T., Yazaki,Y. and Nakamura,Y.
TITLE	Construction of a normalized directionally cloned cDNA library from adult heart and analysis of 3040 clones by partial sequencing
JOURNAL	Genomics 35 (1), 231-235 (1996)
PUBMED	8661126
COMMENT	Contact: Yusuke Nakamura Institute of Medical Science University of Tokyo 4-6-1, Shirokanedai, Minato-ku, Tokyo 108, Japan Tel: 81-3-5449-5372 Fax: 81-3-5449-5433 Email: yusuke@ims.u-tokyo.ac.jp.
FEATURES	Location/Qualifiers
source	1..376 /organism="Homo sapiens" /mol_type="mRNA" /db_xref="taxon:9606" /clone="3NHC5059" /dev_stage="adult" /clone_lib="Human heart cDNA (Ynakamura)" /note="Organ: heart; normalized directionally cloned cDNA from adult heart"
ORIGIN	Query Match 100.0%; Score 159; DB 5; Length 376; Best Local Similarity 100.0%; Pred. No. 8.2e-35; Matches 159; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY	1 ATGGAGAAAGTCCAATACCTCCTCGCTCAGCTATAGAAGAGCGCTCAACATTGAAATG 60
DB	182 ATGGAGAAAGTCCAATACCTCCTCGCTCAGCTATAGAAGAGCGCTCAACATTGAAATG 241
QY	61 CCTCAACAGCAGCTCAAAAGCTACAGAACTATTATCAATTTCTGCTCATCTTAATA 120
DB	242 CCTCAACAGCAGCTCAAAAGCTACAGAACTATTATCAATTTCTGCTCATCTTAATA 301
QY	121 TGTCTCTTGTGATCTGTATCATCGTATGCTTCTCTGA 159
DB	302 TGTCTCTTGTGATCTGTATCATCGTATGCTTCTCTGA 340
RESULT 3	383 bp mRNA linear EST 04-SEP-2003
LOCUS	AL599452 DKFZp313N0529.r1 313 (synonym: hlcc2) Homo sapiens cDNA clone
DEFINITION	DKFZp313N0529_5', mRNA sequence.
ACCESSION	AL599452
VERSION	AL599452.1 GI:15162740
KEYWORDS	EST.
SOURCE	Homo sapiens (human)
ORGANISM	Homo sapiens
	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae; Homo.
REFERENCE	1 (bases 1 to 383)
AUTHORS	Bloeker,H., Boecher,M., Brandt,P., Mewes,W., Weil,B. and Wiemann,S.
TITLE	EST (Bloeker,H., Boecher,M., Brandt,P., Mewes,H.W., Weil,B. and Wiemann,S.)
JOURNAL	Unpublished (1999)
COMMENT	Contact: MIPS

Ingolstaedter Landstr.1, D-85764 Neuherberg, Germany
This is the 5' sequence of the clone insert
Cloned from S. Wiemann, Molecular Genome Analysis, German Cancer
Research Center (DKFZ); Email s.wiemann@dkfz-heidelberg.de;
sequenced by GBF (National Research Centre for Biotechnology Ltd.,
Braunschweig/Germany) within the cDNA sequencing consortium of the
German Genome Project.

No sl sequence available.
This clone (DKFZp313N0529) is available at the RZPD in Berlin.
Please contact the RZPD: Ressourcenzentrum, Heubnerweg 6, 14059
Berlin-Charlottenburg, GERMANY; Email: clone@rzpd.de.

FEATURES
source

Location/Qualifiers
1..383
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="DKFZp313N0529"
/dev_stage="adult"
/lab_host="DH10B"
/clone_lib="313 (synonym: hlcc2)"
/note="Vector: pTriplex2; Site_1: SfiIA; Site_2: SfiIB;
cDNA-collection"

ORIGIN

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Best Local Similarity 100.0%; Pred. No. 8.2e-35;
Matches 159; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ATGAGAAAGTCCAAATACCTCAGCTCGCTCAGCTATAGAAGAGCCTCAACCAATGAAATG 60
DB 143 ATGAGAAAGTCCAAATACCTCAGCTCGCTCAGCTATAGAAGAGCCTCAACCAATGAAATG 202
QY 61 CCTCAACAGCAGTCAAAAGCTACAGAACTATTTATCAATTTCTGCTCATCTTAATA 120
DB 203 CCTCAACAGCAGTCAAAAGCTACAGAACTATTTATCAATTTCTGCTCATCTTAATA 262
QY 121 TGTCTCTTGTGATCTGTATCATCGTATCGTATCGTCTCTCTGA 159
DB 263 TGTCTCTTGTGATCTGTATCATCGTATCGTATCGTCTCTCTGA 301

RESULT 4

AL600669
LOCUS
DEFINITION
DKFZp31302134 r1 313 (synonym: hlcc2) Homo sapiens cDNA clone
AL600669
ACCESSION
VERSION
KEYWORDS
SOURCE
EST.
GI:15164175

Homo sapiens (human)
Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Hominoidea; Homo.

REFERENCE
1 (bases 1 to 408)
Ansorge, W., Wirkner, U., Mewes, W., Weil, B. and Wiemann, S.
EST (Ansorge, W., Wirkner, U., Mewes, W., Weil, B. and Wiemann, S.)
Unpublished (1999)
Contact: MIPS

MIPS
Ingolstaedter Landstr.1, D-85764 Neuherberg, Germany
This is the 5' sequence of the clone insert
Cloned from S. Wiemann, Molecular Genome Analysis, German Cancer
Research Center (DKFZ); Email s.wiemann@dkfz-heidelberg.de;
sequenced by EMBL (European Molecular Biology Laboratories,
Heidelberg/Germany) within the cDNA sequencing consortium of the
German Genome Project.

No sl sequence available.
This clone (DKFZp31302134) is available at the RZPD in Berlin.
Please contact the RZPD: Ressourcenzentrum, Heubnerweg 6, 14059
Berlin-Charlottenburg, GERMANY; Email: clone@rzpd.de.

FEATURES
source

Location/Qualifiers
1..408

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/note="Vector: pTriplex2; Site_1: SfiIA; Site_2: SfiIB;
cDNA-collection"

ORIGIN

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Best Local Similarity 100.0%; Pred. No. 8.3e-35;
Matches 159; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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DB 202 CCTCAACAGCAGTCAAAAGCTACAGAACTATTTATCAATTTCTGCTCATCTTAATA 261
QY 121 TGTCTCTTGTGATCTGTATCATCGTATCGTATCGTCTCTCTGA 159
DB 262 TGTCTCTTGTGATCTGTATCATCGTATCGTATCGTCTCTCTGA 300

RESULT 5

AL601169
LOCUS
DEFINITION
DKFZp313C1140 r1 313 (synonym: hlcc2) Homo sapiens cDNA clone
AL601169
ACCESSION
VERSION
KEYWORDS
SOURCE
EST.
GI:15164675

Homo sapiens (human)
Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Hominoidea; Homo.

REFERENCE
1 (bases 1 to 412)
Bloeker, H., Boecker, M., Brandt, P., Mewes, W., Weil, B. and
Wiemann, S.
EST (Bloeker, H., Boecker, M., Brandt, P., Mewes, W., Weil, B. and
Wiemann, S.)
Unpublished (1999)
Contact: MIPS

MIPS
Ingolstaedter Landstr.1, D-85764 Neuherberg, Germany
This is the 5' sequence of the clone insert
Cloned from S. Wiemann, Molecular Genome Analysis, German Cancer
Research Center (DKFZ); Email s.wiemann@dkfz-heidelberg.de;
sequenced by GBF (National Research Centre for Biotechnology Ltd.,
Braunschweig/Germany) within the cDNA sequencing consortium of the
German Genome Project.

No sl sequence available.
This clone (DKFZp313C1140) is available at the RZPD in Berlin.
Please contact the RZPD: Ressourcenzentrum, Heubnerweg 6, 14059
Berlin-Charlottenburg, GERMANY; Email: clone@rzpd.de.

FEATURES
source

Location/Qualifiers
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/db_xref="taxon:9606"
/clone="DKFZp313C1140"
/dev_stage="adult"
/lab_host="DH10B"
/clone_lib="313 (synonym: hlcc2)"
/note="Vector: pTriplex2; Site_1: SfiIA; Site_2: SfiIB;
cDNA-collection"

ORIGIN

Page 4

Tel: 650 473 8658
Fax: 650 473 7760
Email: rbrandenberger@geron.com
Insert Length: 426 Std Error: 0.00.
Location/Qualifiers
1. 426
/organism="Homo sapiens"
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/tissue_type="embryonic stem cell, retinoic acid and
mitogen-treated hES cell line H7"
/clone_lib="GRN PRENEU"
/note="oligo dT primed, full-length enriched cDNA library
from hES cell line H7 (p29) maintained in feeder-free
conditions. Embryoid bodies were generated in the presence
of all-trans retinoic acid and mitogens."

FEATURES
source

Query Match 100.0%; Score 159; DB 7; Length 426;
Best Local Similarity 100.0%; Pred. No. 8.3e-35;
Matches 159; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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Qy 61 CCTCAACAGCAGCTCAAAAGCTACAGAATCTATTTATCAATTTCTCTCATCTTAATA 120
Db 167 CCTCAACAGCAGCTCAAAAGCTACAGAATCTATTTATCAATTTCTCTCATCTTAATA 226
Qy 121 TGTCTCTTGTGATCTGTATCATCGTATCGTCTCTCTGA 159
Db 227 TGTCTCTTGTGATCTGTATCATCGTATCGTCTCTCTGA 265

ORIGIN

Query Match 100.0%; Score 159; DB 7; Length 426;
Best Local Similarity 100.0%; Pred. No. 8.3e-35;
Matches 159; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 ATGGAGAAAGTCCAAATACCTCAGCTATAGAGAGGCTCAACCATTTGAATG 60
Db 107 ATGGAGAAAGTCCAAATACCTCAGCTATAGAGAGGCTCAACCATTTGAATG 166
Qy 61 CCTCAACAGCAGCTCAAAAGCTACAGAATCTATTTATCAATTTCTCTCATCTTAATA 120
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Qy 121 TGTCTCTTGTGATCTGTATCATCGTATCGTCTCTCTGA 159
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RESULT 9
AL601173

LOCUS AL601173 431 bp mRNA linear EST 04-SEP-2003
DEFINITION DKFZp313C0340 r1 313 (synonym: hlcc2) Homo sapiens cDNA clone
VERSION AL601173
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Hominoidea; Homo.
1 (bases 1 to 431)
Bloeker, H., Boecker, M., Brandt, P., Mewes, W., Weil, B. and
Wiemann, S.
EST (Bloeker, H., Boecker, M., Brandt, P., Mewes, W., Weil, B. and
Wiemann, S.)
Unpublished (1999)
Contact: MIPS
Ingolstaedter Landstr.1, D-85764 Neuherberg, Germany
This is the 5' sequence of the clone insert
Clone from S. Wiemann, Molecular Genome Analysis, German Cancer
Research Center (DKFZ); Email s.wiemann@dkfz-heidelberg.de;
Sequenced by GSF (National Research Centre for Biotechnology Ltd.,
Braunschweig/Germany) within the cDNA sequencing consortium of the
German Genome Project.
No s1 sequence available.
This clone (DKFZp313C0340) is available at the RZPD in Berlin.
Please contact the RZPD: Ressourcenzentrum, Heubnerweg 6, 14059
Berlin-Charlottenburg, GERMANY; Email: clone@rzpd.de.
Location/Qualifiers
1. 431
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="DKFZp313C0340"

REFERENCE
AUTHORS

TITLE
JOURNAL
COMMENT

Ingolstaedter Landstr.1, D-85764 Neuherberg, Germany
This is the 5' sequence of the clone insert
Clone from S. Wiemann, Molecular Genome Analysis, German Cancer
Research Center (DKFZ); Email s.wiemann@dkfz-heidelberg.de;
Sequenced by GSF (National Research Centre for Biotechnology Ltd.,
Braunschweig/Germany) within the cDNA sequencing consortium of the
German Genome Project.
No s1 sequence available.
This clone (DKFZp313C0340) is available at the RZPD in Berlin.
Please contact the RZPD: Ressourcenzentrum, Heubnerweg 6, 14059
Berlin-Charlottenburg, GERMANY; Email: clone@rzpd.de.
Location/Qualifiers
1. 431
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="DKFZp313C0340"

FEATURES
source

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Qy 61 CCTCAACAGCAGCTCAAAAGCTACAGAATCTATTTATCAATTTCTCTCATCTTAATA 120
Db 203 CCTCAACAGCAGCTCAAAAGCTACAGAATCTATTTATCAATTTCTCTCATCTTAATA 262
Qy 121 TGTCTCTTGTGATCTGTATCATCGTATCGTCTCTCTGA 159
Db 263 TGTCTCTTGTGATCTGTATCATCGTATCGTCTCTCTGA 301

ORIGIN

Query Match 100.0%; Score 159; DB 1; Length 433;
Best Local Similarity 100.0%; Pred. No. 8.3e-35;
Matches 159; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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Db 143 ATGGAGAAAGTCCAAATACCTCAGCTATAGAGAGGCTCAACCATTTGAATG 202
Qy 61 CCTCAACAGCAGCTCAAAAGCTACAGAATCTATTTATCAATTTCTCTCATCTTAATA 120
Db 203 CCTCAACAGCAGCTCAAAAGCTACAGAATCTATTTATCAATTTCTCTCATCTTAATA 262
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Db 263 TGTCTCTTGTGATCTGTATCATCGTATCGTCTCTCTGA 301

/dev_stage="adult"
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/note="vector: pTriplex2; Site_1: SfIIA; Site_2: SfiIB;
cDNA-collection"

ORIGIN

Query Match 100.0%; Score 159; DB 1; Length 431;
Best Local Similarity 100.0%; Pred. No. 8.3e-35;
Matches 159; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 ATGGAGAAAGTCCAAATACCTCAGCTATAGAGAGGCTCAACCATTTGAATG 60
Db 143 ATGGAGAAAGTCCAAATACCTCAGCTATAGAGAGGCTCAACCATTTGAATG 202
Qy 61 CCTCAACAGCAGCTCAAAAGCTACAGAATCTATTTATCAATTTCTCTCATCTTAATA 120
Db 203 CCTCAACAGCAGCTCAAAAGCTACAGAATCTATTTATCAATTTCTCTCATCTTAATA 262
Qy 121 TGTCTCTTGTGATCTGTATCATCGTATCGTCTCTCTGA 159
Db 263 TGTCTCTTGTGATCTGTATCATCGTATCGTCTCTCTGA 301

RESULT 10
AL600088

LOCUS AL600088 433 bp mRNA linear EST 04-SEP-2003
DEFINITION DKFZp313C1332 r1 313 (synonym: hlcc2) Homo sapiens cDNA clone
VERSION AL600088
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Hominoidea; Homo.
1 (bases 1 to 433)
Bloeker, H., Boecker, M., Brandt, P., Mewes, W., Weil, B. and
Wiemann, S.
EST (Bloeker, H., Boecker, M., Brandt, P., Mewes, W., Weil, B. and
Wiemann, S.)
Unpublished (1999)
Contact: MIPS
Ingolstaedter Landstr.1, D-85764 Neuherberg, Germany
This is the 5' sequence of the clone insert
Clone from S. Wiemann, Molecular Genome Analysis, German Cancer
Research Center (DKFZ); Email s.wiemann@dkfz-heidelberg.de;
Sequenced by GSF (National Research Centre for Biotechnology Ltd.,
Braunschweig/Germany) within the cDNA sequencing consortium of the
German Genome Project.
No s1 sequence available.
This clone (DKFZp313C1332) is available at the RZPD in Berlin.
Please contact the RZPD: Ressourcenzentrum, Heubnerweg 6, 14059
Berlin-Charlottenburg, GERMANY; Email: clone@rzpd.de.
Location/Qualifiers
1. 433
/organism="Homo sapiens"
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/db_xref="taxon:9606"
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/clone_lib="313 (synonym: hlcc2)"
/note="vector: pTriplex2; Site_1: SfIIA; Site_2: SfiIB;
cDNA-collection"

FEATURES
source

Ingolstaedter Landstr.1, D-85764 Neuherberg, Germany
This is the 5' sequence of the clone insert
Clone from S. Wiemann, Molecular Genome Analysis, German Cancer
Research Center (DKFZ); Email s.wiemann@dkfz-heidelberg.de;
Sequenced by GSF (National Research Centre for Biotechnology Ltd.,
Braunschweig/Germany) within the cDNA sequencing consortium of the
German Genome Project.
No s1 sequence available.
This clone (DKFZp313C1332) is available at the RZPD in Berlin.
Please contact the RZPD: Ressourcenzentrum, Heubnerweg 6, 14059
Berlin-Charlottenburg, GERMANY; Email: clone@rzpd.de.
Location/Qualifiers
1. 433
/organism="Homo sapiens"
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/note="vector: pTriplex2; Site_1: SfIIA; Site_2: SfiIB;
cDNA-collection"

ORIGIN

Query Match 100.0%; Score 159; DB 1; Length 433;
Best Local Similarity 100.0%; Pred. No. 8.3e-35;
Matches 159; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 ATGGAGAAAGTCCAAATACCTCAGCTATAGAGAGGCTCAACCATTTGAATG 60
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Db 203 CCTCAACAGCAGCTCAAAAGCTACAGAATCTATTTATCAATTTCTCTCATCTTAATA 262
Qy 121 TGTCTCTTGTGATCTGTATCATCGTATCGTCTCTCTGA 159
Db 263 TGTCTCTTGTGATCTGTATCATCGTATCGTCTCTCTGA 301


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SOURCE      Homo sapiens (human)
ORGANISM    Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
            Hominidae; Homo.
REFERENCE   1 (bases 1 to 448)
AUTHORS    Tanaka,T., Ogiwara,A., Uchiyama,I., Takagi,T., Yazaki,Y. and
            Nakamura,Y.
TITLE      Construction of a normalized directionally cloned cDNA library from
            adult heart and analysis of 3040 clones by partial sequencing
JOURNAL    Genomics 35 (1), 231-235 (1996)
PUBMED     8661126
COMMENT    Contact: Yusuke Nakamura
            Institute of Medical Science
            University of Tokyo
            4-6-1, Shirokanedai, Minato-ku, Tokyo 108, Japan
            Tel: 81-3-5449-5372
            Fax: 81-3-5449-5433
            Email: yusuke@ims.u-tokyo.ac.jp.
            Location/Qualifiers
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FEATURES             source
ORIGIN
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DB      184 ATGGAGAAAGTCCAATACCTCACTCGCTCAGCTATAGAGAGCGCTCAACCATTTGAATG 243
QY      61  CCTCAACAGCAGCTCAAAAGCTACAGAACTCTATTTATCAATTTCTGTCATCTTAATA 120
DB      244 CCTCAACAGCAGCTCAAAAGCTACAGAACTCTATTTATCAATTTCTGTCATCTTAATA 303
QY      121 TGTCTCTTGTGATCTGTATCATCGTGATGCTTCTCTGA 159
DB      304 TGTCTCTTGTGATCTGTATCATCGTGATGCTTCTCTGA 342

RESULT 14
C04050
LOCUS      C04050 Human heart cDNA-(Ynakamura) Homo sapiens cDNA clone
DEFINITION 3NHCl2620, mRNA sequence.
ACCESSION  C04050
VERSION     C04050.1 GI:1467301
KEYWORDS   EST.
SOURCE     Homo sapiens (human)
ORGANISM   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
            Hominidae; Homo.
REFERENCE   1 (bases 1 to 451)
AUTHORS    Tanaka,T., Ogiwara,A., Uchiyama,I., Takagi,T., Yazaki,Y. and
            Nakamura,Y.
TITLE      Construction of a normalized directionally cloned cDNA library from
            adult heart and analysis of 3040 clones by partial sequencing
JOURNAL    Genomics 35 (1), 231-235 (1996)
PUBMED     8661126
COMMENT    Contact: Yusuke Nakamura
            Institute of Medical Science
            University of Tokyo
            4-6-1, Shirokanedai, Minato-ku, Tokyo 108, Japan
            Tel: 81-3-5449-5372

FEATURES             source
ORIGIN
Query Match      100.0%; Score 159; DB 5; Length 448;
Best Local Similarity 100.0%; Pred. No. 8.4e-35;
Matches 159; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1  ATGGAGAAAGTCCAATACCTCACTCGCTCAGCTATAGAGAGCGCTCAACCATTTGAATG 60
DB      184 ATGGAGAAAGTCCAATACCTCACTCGCTCAGCTATAGAGAGCGCTCAACCATTTGAATG 243
QY      61  CCTCAACAGCAGCTCAAAAGCTACAGAACTCTATTTATCAATTTCTGTCATCTTAATA 120
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DB      304 TGTCTCTTGTGATCTGTATCATCGTGATGCTTCTCTGA 342

RESULT 15
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LOCUS      AL601166
DEFINITION DKFp313B0340 r1 313 (synonym: hlcc2) Homo sapiens cDNA clone
ACCESSION  AL601166
VERSION     AL601166
KEYWORDS   EST.
SOURCE     Homo sapiens (human)
ORGANISM   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
            Hominidae; Homo.
REFERENCE   1 (bases 1 to 455)
AUTHORS    Bloecker,H., Boecher,M., Brandt,P., Mewes,W., Weil,B. and
            Wiemann,S.
TITLE      EST (Bloecker,H., Boecher,M., Brandt,P., Mewes,W., Weil,B. and
            Wiemann,S.)
JOURNAL    Unpublished (1999)
COMMENT    Contact: MIPS
            MIPS
            Ingolstaedter Landstr.1, D-85764 Neuherberg, Germany
            This is the 5' sequence of the clone insert
            Clone from S. Wiemann, Molecular Genome Analysis, German Cancer
            Research Center (DKFZ); Email s.wiemann@dkfz-heidelberg.de;
            sequenced by GBF (National Research Centre for Biotechnology Ltd.,
            Braunschweig/Germany) within the cDNA sequencing consortium of the
            German Genome Project.
            No sl sequence available.
            This clone (DKFp313B0340) is available at the RZPD in Berlin.
            Please contact the RZPD: Ressourcenzentrum, Heubnerweg 6, 14059
            Berlin-Charlottenburg, GERMANY; Email: clone@rzpd.de.
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                /lab_host="DH10B"
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FEATURES             source
ORIGIN
Query Match      100.0%; Score 159; DB 5; Length 451;
Best Local Similarity 100.0%; Pred. No. 8.4e-35;
Matches 159; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1  ATGGAGAAAGTCCAATACCTCACTCGCTCAGCTATAGAGAGCGCTCAACCATTTGAATG 60
DB      161 ATGGAGAAAGTCCAATACCTCACTCGCTCAGCTATAGAGAGCGCTCAACCATTTGAATG 220
QY      61  CCTCAACAGCAGCTCAAAAGCTACAGAACTCTATTTATCAATTTCTGTCATCTTAATA 120
DB      221 CCTCAACAGCAGCTCAAAAGCTACAGAACTCTATTTATCAATTTCTGTCATCTTAATA 280
QY      121 TGTCTCTTGTGATCTGTATCATCGTGATGCTTCTCTGA 159
DB      281 TGTCTCTTGTGATCTGTATCATCGTGATGCTTCTCTGA 319

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ORIGIN		cDNA-collection"	
Query Match		100.0%; Score 159; DB 1; Length 455;	
Best Local Similarity		100.0%; Pred. No. 8.4e-35;	
Matches 159; Conservative		0; Mismatches 0; Indels 0; Gaps 0;	
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DB	142	ATGGAGAAAGTCCATACCTCACTCGCTCAGCTATAAGAGAGCCTCAACCAATTGAAATG	201
QY	61	CCTCAACAGCAGCTCAAAAGCTACAGAACTATTATCAATTTCTGCTCATCTTAATA	120
DB	202	CCTCAACAGCAGCTCAAAAGCTACAGAACTATTATCAATTTCTGCTCATCTTAATA	261
QY	121	TGCTCTTGTGATCTGTATATCATCGATGCTTCTCTGA	159
DB	262	TGCTCTTGTGATCTGTATATCATCGATGCTTCTCTGA	300
RESULT 16			
AL599208		477 bp mRNA linear EST 04-SEP-2003	
LOCUS			
DEFINITION		DKFZp313D2225 r1 313 (synonym: hlcc2) Homo sapiens cDNA clone	
ACCESSION		DKFZp313D2225 5', mRNA sequence.	
VERSION		AL599208	
KEYWORDS		EST.	
SOURCE		AL599208.1 GI:15162496	
ORGANISM		Homo sapiens (human)	
REFERENCE		1 (bases 1 to 477)	
AUTHORS		Poustka,A., Wellenreuther,R., Mewes,H.W., Weil,B. and Wiemann,S.).	
TITLE		EST (Poustka,A., Wellenreuther,R., Mewes,H.W., Weil,B. and Wiemann,S.)	
JOURNAL		Unpublished (1999)	
COMMENT		Contact: MIPS	
FEATURES		Location/Qualifiers	
source		1..477	
		/organism="Homo sapiens"	
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		/dev_stage="adult"	
		/lab_host="DH10B"	
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Best Local Similarity		100.0%; Pred. No. 8.5e-35;	
Matches 159; Conservative		0; Mismatches 0; Indels 0; Gaps 0;	
QY	1	ATGGAGAAAGTCCATACCTCACTCGCTCAGCTATAAGAGAGCCTCAACCAATTGAAATG	60
DB	201	ATGGAGAAAGTCCATACCTCACTCGCTCAGCTATAAGAGAGCCTCAACCAATTGAAATG	260
QY	61	CCTCAACAGCAGCTCAAAAGCTACAGAACTATTATCAATTTCTGCTCATCTTAATA	120

DB	261	CCTCAACAGCAGCTCAAAAGCTACAGAACTATTATCAATTTCTGCTCATCTTAATA	320
QY	121	TGCTCTTGTGATCTGTATATCATCGTGTGATGCTTCTCTGA	159
DB	321	TGCTCTTGTGATCTGTATATCATCGTGTGATGCTTCTCTGA	359
RESULT 17			
AL600135		478 bp mRNA linear EST 04-SEP-2003	
LOCUS			
DEFINITION		DKFZp313F1932 r1 313 (synonym: hlcc2) Homo sapiens cDNA clone	
ACCESSION		DKFZp313F1932 5', mRNA sequence.	
VERSION		AL600135	
KEYWORDS		EST.	
SOURCE		AL600135.1 GI:15163446	
ORGANISM		Homo sapiens (human)	
REFERENCE		1 (bases 1 to 478)	
AUTHORS		Bloeker,H., Boecker,M., Brandt,P., Mewes,M., Weil,B. and Wiemann,S.).	
TITLE		EST (Bloeker,H., Boecker,M., Brandt,P., Mewes,H.W., Weil,B. and Wiemann,S.)	
JOURNAL		Unpublished (1999)	
COMMENT		Contact: MIPS	
FEATURES		Location/Qualifiers	
source		1..478	
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		/lab_host="DH10B"	
		/clone_lib="313 (synonym: hlcc2)"	
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Query Match		100.0%; Score 159; DB 1; Length 478;	
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Matches 159; Conservative		0; Mismatches 0; Indels 0; Gaps 0;	
QY	1	ATGGAGAAAGTCCATACCTCACTCGCTCAGCTATAAGAGAGCCTCAACCAATTGAAATG	60
DB	142	ATGGAGAAAGTCCATACCTCACTCGCTCAGCTATAAGAGAGCCTCAACCAATTGAAATG	201
QY	61	CCTCAACAGCAGCTCAAAAGCTACAGAACTATTATCAATTTCTGCTCATCTTAATA	120
DB	202	CCTCAACAGCAGCTCAAAAGCTACAGAACTATTATCAATTTCTGCTCATCTTAATA	261
QY	121	TGCTCTTGTGATCTGTATATCATCGTGTGATGCTTCTCTGA	159
DB	262	TGCTCTTGTGATCTGTATATCATCGTGTGATGCTTCTCTGA	300
RESULT 18			
AL601279		479 bp mRNA linear EST 04-SEP-2003	
LOCUS			

DEFINITION DKFZp331L1640_r1 313 (synonym: hlcc2) Homo sapiens cDNA clone
 ACCESSION DKFZp331L1640 5', mRNA sequence.
 VERSION AL601279
 KEYWORDS EST.
 SOURCE Homo sapiens (human)
 ORGANISM Homo sapiens

REFERENCE
 AUTHORS Bloeker, H., Boecker, H., Boecker, M., Brandt, P., Mewes, W., Weil, B. and Wiemann, S.
 TITLE EST (Bloeker, H., Boecker, H., Boecker, M., Brandt, P., Mewes, W., Weil, B. and Wiemann, S.)
 JOURNAL Unpublished (1999)
 COMMENT Contact: MIPS

FEATURES
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 1..479
 /organism="Homo sapiens"
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 /db_xref="taxon:9606"
 /clone="DKFZp331L1640"
 /dev_stage="adult"
 /lab_host="DH10B"
 /clone_lib="313 (synonym: hlcc2)"
 /notes="vector: pTriplex2; Site_1: SfIIA; Site_2: SfiIB;
 cDNA-collection"

ORIGIN
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 Best Local Similarity 100.0%; Pred. No. 8.5e-35;
 Matches 159; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ATGGAGAAAGTCCAAATACCTCAGCTCAGCTATAGAGAGCGCTCAACCATTTGAATG 60
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 Db 196 ATGGAGAAAGTCCAAATACCTCAGCTCAGCTATAGAGAGCGCTCAACCATTTGAATG 255
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QY 61 CCTCAACAGCAGCTCAAAAGCTACAGAACTCTATTATCAATTTCTGCTCATCTTAATA 120
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 Db 256 CCTCAACAGCAGCTCAAAAGCTACAGAACTCTATTATCAATTTCTGCTCATCTTAATA 315
 |||||

QY 121 TGTCTCTTGTGATCTGTATCATCGTGATGCTTCTCTGA 159
 |||||
 Db 316 TGTCTCTTGTGATCTGTATCATCGTGATGCTTCTCTGA 354
 |||||

RESULT 19
 AL601190
 LOCUS DKFZp331D0840_r1 313 (synonym: hlcc2) Homo sapiens cDNA clone
 DEFINITION DKFZp331D0840 5', mRNA sequence.
 ACCESSION AL601190
 VERSION AL601190
 KEYWORDS EST.
 SOURCE Homo sapiens (human)
 ORGANISM Homo sapiens

REFERENCE
 AUTHORS Bloeker, H., Boecker, H., Boecker, M., Brandt, P., Mewes, W., Weil, B. and Wiemann, S.
 TITLE EST (Bloeker, H., Boecker, H., Boecker, M., Brandt, P., Mewes, W., Weil, B. and Wiemann, S.)
 JOURNAL Unpublished (1999)
 COMMENT Contact: MIPS

FEATURES
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 /organism="Homo sapiens"
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 /clone="DKFZp331D0840"
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 Matches 159; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ATGGAGAAAGTCCAAATACCTCAGCTCAGCTATAGAGAGCGCTCAACCATTTGAATG 60
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 Db 196 ATGGAGAAAGTCCAAATACCTCAGCTCAGCTATAGAGAGCGCTCAACCATTTGAATG 255
 |||||

QY 61 CCTCAACAGCAGCTCAAAAGCTACAGAACTCTATTATCAATTTCTGCTCATCTTAATA 120
 |||||
 Db 256 CCTCAACAGCAGCTCAAAAGCTACAGAACTCTATTATCAATTTCTGCTCATCTTAATA 315
 |||||

QY 121 TGTCTCTTGTGATCTGTATCATCGTGATGCTTCTCTGA 159
 |||||
 Db 316 TGTCTCTTGTGATCTGTATCATCGTGATGCTTCTCTGA 354
 |||||

RESULT 20
 AJ708798
 LOCUS AJ708798 CPMF01 Homo sapiens cDNA clone CPMF03862, mRNA sequence.
 DEFINITION AJ708798
 ACCESSION AJ708798
 VERSION AJ708798.1 GI:49503093
 KEYWORDS EST.
 SOURCE Homo sapiens (human)
 ORGANISM Homo sapiens

REFERENCE
 AUTHORS Millino, C.
 TITLE Expression profiling of human hypertrophic cardiomyopathy progressed to dilated cardiomyopathy by DNA microarray analysis
 JOURNAL Unpublished (2004)
 COMMENT Contact: Millino C
 BIOLOGY and CRIBI
 University of Padova
 Via U. Bassi, 58/B, 35131, ITALY.
 Location/Qualifiers
 1..533
 /organism="Homo sapiens"
 /mol_type="mRNA"

AUTHORS Bloeker, H., Boecker, H., Boecker, M., Brandt, P., Mewes, W., Weil, B. and Wiemann, S.
 TITLE EST (Bloeker, H., Boecker, H., Boecker, M., Brandt, P., Mewes, H.W., Weil, B. and Wiemann, S.)
 JOURNAL Unpublished (1999)
 COMMENT Contact: MIPS

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 /organism="Homo sapiens"
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 /dev_stage="adult"
 /lab_host="DH10B"
 /clone_lib="313 (synonym: hlcc2)"
 /notes="vector: pTriplex2; Site_1: SfIIA; Site_2: SfiIB;
 cDNA-collection"

ORIGIN
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 Best Local Similarity 100.0%; Pred. No. 8.5e-35;
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QY 1 ATGGAGAAAGTCCAAATACCTCAGCTCAGCTATAGAGAGCGCTCAACCATTTGAATG 60
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 Db 196 ATGGAGAAAGTCCAAATACCTCAGCTCAGCTATAGAGAGCGCTCAACCATTTGAATG 255
 |||||

QY 61 CCTCAACAGCAGCTCAAAAGCTACAGAACTCTATTATCAATTTCTGCTCATCTTAATA 120
 |||||
 Db 256 CCTCAACAGCAGCTCAAAAGCTACAGAACTCTATTATCAATTTCTGCTCATCTTAATA 315
 |||||

QY 121 TGTCTCTTGTGATCTGTATCATCGTGATGCTTCTCTGA 159
 |||||
 Db 316 TGTCTCTTGTGATCTGTATCATCGTGATGCTTCTCTGA 354
 |||||

RESULT 20
 AJ708798
 LOCUS AJ708798 CPMF01 Homo sapiens cDNA clone CPMF03862, mRNA sequence.
 DEFINITION AJ708798
 ACCESSION AJ708798
 VERSION AJ708798.1 GI:49503093
 KEYWORDS EST.
 SOURCE Homo sapiens (human)
 ORGANISM Homo sapiens

REFERENCE
 AUTHORS Millino, C.
 TITLE Expression profiling of human hypertrophic cardiomyopathy progressed to dilated cardiomyopathy by DNA microarray analysis
 JOURNAL Unpublished (2004)
 COMMENT Contact: Millino C
 BIOLOGY and CRIBI
 University of Padova
 Via U. Bassi, 58/B, 35131, ITALY.
 Location/Qualifiers
 1..533
 /organism="Homo sapiens"
 /mol_type="mRNA"


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/db_xref="taxon:9606"
/clone="CMPD03862"
/tissue_type="heart"
/clone_lib="CMPD01"
/note="caucasian"

ORIGIN
Query Match          100.0%; Score 159; DB 1; Length 533;
Best Local Similarity 100.0%; Pred. No. 8.6e-35;
Matches 159; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 ATGGAGAAGTCCAATACCTCAGTCGCTAAGAGAGCGCTCAACCATTTGAATG 60
        |||
Db       168 ATGGAGAAGTCCAATACCTCAGTCGCTAAGAGAGCGCTCAACCATTTGAATG 227
        |||

QY      61 CCTCAACAGACGCTCAAAGCTACAGAACTATTATTCATTTCTGTCTCATCTTAATA 120
        |||
Db       228 CCTCAACAGACGCTCAAAGCTACAGAACTATTATTCATTTCTGTCTCATCTTAATA 287
        |||

QY      121 TGTCTTCTTGCTGATCTGTATCATCGTATCATCGTATCTTCTCTGA 159
        |||
Db       288 TGTCTTCTTGCTGATCTGTATCATCGTATCATCGTATCTTCTCTGA 326
        |||

RESULT 21
C03682
LOCUS           C03682 Human heart cDNA (YNakamura) Homo sapiens CDNA clone
DEFINITION     3NHC2016, mRNA sequence.
ACCESSION     C03682
VERSION       C03682.1 GI:1466933
KEYWORDS      EST.
SOURCE        Homo sapiens (human)
ORGANISM      Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
              Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
              Homnidae; Homo.
REFERENCE      1 (bases 1 to 533)
AUTHORS       Tanaka,T., Ogiwara,A., Uchiyama,I., Takagi,T., Yazaki,Y. and
              Nakamura,Y.
TITLE         Construction of a normalized directionally cloned cDNA library from
              adult heart and analysis of 3040 clones by partial sequencing
JOURNAL       Genomics 35 (1), 231-235 (1996)
PUBMED       8661126
COMMENT       Contact: Yusuke Nakamura
              Institute of Medical Science
              University of Tokyo
              4-6-1, Shirokanedai, Minato-ku, Tokyo 108, Japan
              Tel: 81-3-5449-5372
              Fax: 81-3-5449-5433
              Email: yusuke@ims.u-tokyo.ac.jp.
              Location/Qualifiers
                1..533
                  /organism="Homo sapiens"
                  /mol_type="mRNA"
                  /db_xref="taxon:9606"
                  /clone="3NHC2016"
                  /dev stage="adult"
                  /clone_lib="Human heart cDNA (YNakamura)"
                  /note="Organ: heart; normalized directionally cloned cDNA
                  from adult heart"

FEATURES             source
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                     /tissue_type="heart"
                     /clone_lib="CMPD01"
                     /note="caucasian"

ORIGIN
Query Match          100.0%; Score 159; DB 5; Length 533;
Best Local Similarity 100.0%; Pred. No. 8.6e-35;
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QY      1 ATGGAGAAGTCCAATACCTCAGTCGCTAAGAGAGCGCTCAACCATTTGAATG 60
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Db       185 ATGGAGAAGTCCAATACCTCAGTCGCTAAGAGAGCGCTCAACCATTTGAATG 244
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QY      61 CCTCAACAGACGCTCAAAGCTACAGAACTATTATTCATTTCTGTCTCATCTTAATA 120
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|||||

224 CCTCAACAGCAGCTCAAAAGCTACAGAACTATTATCAATTTCTGCTCATCTTAATA 283

QY 121 TGTCTCTGCTGATCTGATATCATCTGATGATGCTTCTCTGA 159

|||||

284 TGTCTCTGCTGATCTGATATCATCTGATGCTTCTCTGA 322

|||||

RESULT 26

AL600489 547 bp mRNA linear EST 04-SEP-2003

LOCUS DKFP31302033 r1 313 (synonym: hlcc2) Homo sapiens cDNA clone

DEFINITION DKFP31302033-5', mRNA sequence.

ACCESSION AL600489

VERSION AL600489.1 GI:15163995

KEYWORDS EST.

SOURCE Homo sapiens (human)

ORGANISM Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae; Homo.

REFERENCE 1 (bases 1 to 547)

AUTHORS Koehler,K., Beyer,A., Mewes,W., Weil,B. and Wiemann,S.

TITLE EST (Koehler,K., Beyer,A., Mewes,W., Weil,B. and Wiemann,S.)

JOURNAL Unpublished (1999)

COMMENT Contact: MIPS

MIPS Ingolstaedter Landstr.1, D-85764 Neuherberg, Germany

This is the 5' sequence of the clone insert

Clone from S. Wiemann, Molecular Genome Analysis, German Cancer Research Center (DKFZ); Email s.wiemann@dkfz-heidelberg.de;

sequenced by BNFZ (Biomedical Research Center at the Charite, Berlin/Germany) within the cDNA sequencing consortium of the German Genome Project.

No 5' sequence available.

This clone (DKFP31302033) is available at the RZPD in Berlin.

Please contact the RZPD: Ressourcenzentrum, Heubnerweg 6, 14059 Berlin-Charlottenburg, GERMANY; Email: clone@rzpd.de.

Location/Qualifiers

1. .547

/organism="Homo sapiens"

/mol_type="mRNA"

/db_xref="taxon:9606"

/clone="DKFP31302033"

/dev_stage="adult"

/lab_host="DH10B"

/clone_lib="313 (synonym: hlcc2)"

/notes="Vector: pTriplex2; Site_1: SfiIA; Site_2: SfiIB; cDNA-collection"

FEATURES

source

1. .547

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/mol_type="mRNA"

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/notes="Vector: pTriplex2; Site_1: SfiIA; Site_2: SfiIB; cDNA-collection"

ORIGIN

Query Match 100.0%; Score 159; DB 1; Length 547;

Best Local Similarity 100.0%; Pred. No. 8.7e-35;

Matches 159; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ATGGAGAAAGTCCATACCTCAGCTCAGCTATAGAGAGCGCTCAACCATTTGAATG 60

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207 ATGGAGAAAGTCCATACCTCAGCTCAGCTATAGAGAGCGCTCAACCATTTGAATG 266

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61 CCTCAACAGCAGCTCAAAAGCTACAGAACTATTATCAATTTCTGCTCATCTTAATA 120

|||||

267 CCTCAACAGCAGCTCAAAAGCTACAGAACTATTATCAATTTCTGCTCATCTTAATA 326

|||||

121 TGTCTCTGCTGATCTGATATCATCTGATGCTTCTCTGA 159

|||||

327 TGTCTCTGCTGATCTGATATCATCTGATGCTTCTCTGA 365

|||||

RESULT 27

AJ708988 548 bp mRNA linear EST 30-JUN-2004

LOCUS AJ708988

DEFINITION AJ708988 CMPD01 Homo sapiens cDNA clone CMPD04183, mRNA sequence.

ACCESSION AJ708988

AJ708988.1 GI:49503283

EST.

KEYWORDS Homo sapiens (human)

SOURCE Homo sapiens

ORGANISM Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae; Homo.

REFERENCE 1 (bases 1 to 548)

AUTHORS Millino,C.

TITLE Expression profiling of human hypertrophic cardiomyopathy progressed to dilated cardiomyopathy by DNA microarray analysis

JOURNAL Unpublished (2004)

COMMENT Contact: Millino C

Biologiy and CRIBI

University of Padova

Via U. Bassi, 58/B, 35131, ITALY.

Location/Qualifiers

1. .548

/organism="Homo sapiens"

/mol_type="mRNA"

/db_xref="taxon:9606"

/clone="CMPD04183"

/tissue_type="heart"

/clone_lib="CMPD01"

/note="caucasian"

ORIGIN

Query Match 100.0%; Score 159; DB 1; Length 548;

Best Local Similarity 100.0%; Pred. No. 8.7e-35;

Matches 159; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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195 ATGGAGAAAGTCCATACCTCAGCTCAGCTATAGAGAGCGCTCAACCATTTGAATG 254

|||||

61 CCTCAACAGCAGCTCAAAAGCTACAGAACTATTATCAATTTCTGCTCATCTTAATA 120

|||||

255 CCTCAACAGCAGCTCAAAAGCTACAGAACTATTATCAATTTCTGCTCATCTTAATA 314

|||||

121 TGTCTCTGCTGATCTGATATCATCTGATGCTTCTCTGA 159

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315 TGTCTCTGCTGATCTGATATCATCTGATGCTTCTCTGA 353

|||||

RESULT 28

BP257178 550 bp mRNA linear EST 16-SEP-2004

LOCUS BP257178 Sugano cDNA library, heart Homo sapiens cDNA clone

DEFINITION HRT00312, mRNA sequence.

ACCESSION BP257178

VERSION BP257178.1 GI:52172408

KEYWORDS EST.

SOURCE Homo sapiens (human)

ORGANISM Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae; Homo.

REFERENCE 1 (bases 1 to 550)

AUTHORS Suzuki,Y., Yamashita,R., Shiota,M., Sakakibara,Y., Chiba,J., Mizushima-Sugano,J., Nakai,K. and Sugano,S.

TITLE Sequence comparison of human and mouse genes reveals a homologous block structure in the promoter regions

JOURNAL Genome Res. 14 (9), 1711-1718 (2004)

COMMENT 15342556

Contact: Yutaka Suzuki

Department of Virology

Institute of Medical Science, University of Tokyo

4-6-1, Shirokanedai, Minatoku, Tokyo 108-8639, Japan

Email: yasuku@ims.u-tokyo.ac.jp.

Location/Qualifiers

1. .550

/organism="Homo sapiens"

/mol_type="mRNA"

FEATURES

source

1. .550

/organism="Homo sapiens"

/mol_type="mRNA"

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/clone="HRT00312"
/tissue_type="heart"
/clone_lib="Sugano cDNA library, heart"

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Query Match
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Matches 159; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ATGGAGAAGTCCAAATACCTCACTCGCTCAGCTATAGAAGAGCCTCAACCAATGAAATG 60
DB 194 ATGGAGAAGTCCAAATACCTCACTCGCTCAGCTATAGAAGAGCCTCAACCAATGAAATG 253

QY 61 CCTCAACAGCAGCTCAAAAGCTACAGAACTATTTATCAATTTCTGCTCATCTTAATA 120
DB 254 CCTCAACAGCAGCTCAAAAGCTACAGAACTATTTATCAATTTCTGCTCATCTTAATA 313

QY 121 TGTCTCTTCTGATCTGATCATCGTATCATCGTATCGTCTCTGA 159
DB 314 TGTCTCTTCTGATCTGATCATCGTATCATCGTATCGTCTCTGA 352

RESULT 29
BP259966
LOCUS
DEFINITION
BP259966 Sugano cDNA library, heart Homo sapiens cDNA clone
HRT08389, mRNA sequence.
ACCESSION
BP259966
VERSION
BP259966.1 GI:52175196
KEYWORDS
EST.
SOURCE
Homo sapiens (human)
ORGANISM
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Hominidae; Homo.
1 (bases 1 to 550)
Suzuki, Y., Yamashita, R., Shiota, M., Sakakibara, Y., Chiba, J.,
Mizushima-Sugano, J., Nakai, K. and Sugano, S.
Sequence comparison of human and mouse genes reveals a homologous
block structure in the promoter regions
Genome Res. 14 (9), 1711-1718 (2004)
15342556
Contact: Yutaka Suzuki
Department of Virology
Institute of Medical Science, University of Tokyo
4-6-1, Shirokanedai, Minatoku, Tokyo 108-8639, Japan
Email: yuzuki@ims.u-tokyo.ac.jp.

FEATURES
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1..550
/organism="Homo sapiens"
/mol_type="mRNA"
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/clone="HRT08389"
/tissue_type="heart"
/clone_lib="Sugano cDNA library, heart"

ORIGIN

Query Match
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DB 195 ATGGAGAAGTCCAAATACCTCACTCGCTCAGCTATAGAAGAGCCTCAACCAATGAAATG 254

QY 61 CCTCAACAGCAGCTCAAAAGCTACAGAACTATTTATCAATTTCTGCTCATCTTAATA 120
DB 255 CCTCAACAGCAGCTCAAAAGCTACAGAACTATTTATCAATTTCTGCTCATCTTAATA 314

QY 121 TGTCTCTTCTGATCTGATCATCGTATCATCGTATCGTCTCTGA 159
DB 315 TGTCTCTTCTGATCTGATCATCGTATCATCGTATCGTCTCTGA 353

RESULT 31
BP260274
LOCUS
DEFINITION
BP260274 Sugano cDNA library, heart Homo sapiens cDNA clone
HRT09384, mRNA sequence.
ACCESSION
BP260274
VERSION
BP260274.1 GI:52175505
KEYWORDS
EST.
SOURCE
Homo sapiens (human)
ORGANISM
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Hominidae; Homo.
1 (bases 1 to 550)
Suzuki, Y., Yamashita, R., Shiota, M., Sakakibara, Y., Chiba, J.,
Mizushima-Sugano, J., Nakai, K. and Sugano, S.
Sequence comparison of human and mouse genes reveals a homologous
block structure in the promoter regions
Genome Res. 14 (9), 1711-1718 (2004)

/db_xref="taxon:9606"
/clone="HRT00312"
/tissue_type="heart"
/clone_lib="Sugano cDNA library, heart"

ORIGIN

Query Match
Best Local Similarity 100.0%; Score 159; DB 3; Length 550;
Matches 159; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ATGGAGAAGTCCAAATACCTCACTCGCTCAGCTATAGAAGAGCCTCAACCAATGAAATG 60
DB 195 ATGGAGAAGTCCAAATACCTCACTCGCTCAGCTATAGAAGAGCCTCAACCAATGAAATG 254

QY 61 CCTCAACAGCAGCTCAAAAGCTACAGAACTATTTATCAATTTCTGCTCATCTTAATA 120
DB 255 CCTCAACAGCAGCTCAAAAGCTACAGAACTATTTATCAATTTCTGCTCATCTTAATA 314

QY 121 TGTCTCTTCTGATCTGATCATCGTATCATCGTATCGTCTCTGA 159
DB 315 TGTCTCTTCTGATCTGATCATCGTATCATCGTATCGTCTCTGA 353

RESULT 31
BP260274
LOCUS
DEFINITION
BP260274 Sugano cDNA library, heart Homo sapiens cDNA clone
HRT09384, mRNA sequence.
ACCESSION
BP260274
VERSION
BP260274.1 GI:52175505
KEYWORDS
EST.
SOURCE
Homo sapiens (human)
ORGANISM
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Hominidae; Homo.
1 (bases 1 to 550)
Suzuki, Y., Yamashita, R., Shiota, M., Sakakibara, Y., Chiba, J.,
Mizushima-Sugano, J., Nakai, K. and Sugano, S.
Sequence comparison of human and mouse genes reveals a homologous
block structure in the promoter regions
Genome Res. 14 (9), 1711-1718 (2004)

```
15342556
Contact: Yutaka Suzuki
Department of Virology
Institute of Medical Science, University of Tokyo
4-6-1, Shirokanedai, Minatoku, Tokyo 108-8639, Japan
Email: yusuzuki@ims.u-tokyo.ac.jp.

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QY 1 ATGGAGAAAGTCCCAATACCTCAGCTCAGCTATAGAAGAGCCTCAACCAATTGAAATG 60
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QY 61 CCTCAACAAGCAGCTCAAAAGCTACAGAATCTATTTATCAATTTCTGCTCATCTTAATA 120
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QY 121 TGTCTCTTGTGATCTGTATCATCGTGATGCTTCTCTGA 159
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Db 283 TGTCTCTTGTGATCTGTATCATCGTGATGCTTCTCTGA 321
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RESULT 32
BP259171
LOCUS
DEFINITION
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    HRT05807, mRNA sequence.
ACCESSION
    BP259171
VERSION
    BP259171.1 GI:52174401
KEYWORDS
    EST.
SOURCE
    Homo sapiens (human)
ORGANISM
    Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
    Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
    Homnidae; Homo.
REFERENCE
    1 (bases 1 to 551)
    Suzuki,Y., Yamashita,R., Shirota,M., Sakakibara,Y., Chiba,J.,
    Mizushima-Sugano,J., Nakai,K. and Sugano,S.
    Sequence comparison of human and mouse genes reveals a homologous
    block structure in the promoter regions
    Genome Res. 14 (9), 1711-1718 (2004)
JOURNAL
    PUBMED
    15342556
COMMENT
    Contact: Yutaka Suzuki
    Department of Virology
    Institute of Medical Science, University of Tokyo
    4-6-1, Shirokanedai, Minatoku, Tokyo 108-8639, Japan
    Email: yusuzuki@ims.u-tokyo.ac.jp.

FEATURES
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        /tissue_type="heart"
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QY 1 ATGGAGAAAGTCCCAATACCTCAGCTCAGCTATAGAAGAGCCTCAACCAATTGAAATG 60
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QY 61 CCTCAACAAGCAGCTCAAAAGCTACAGAATCTATTTATCAATTTCTGCTCATCTTAATA 120
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QY 121 TGTCTCTTGTGATCTGTATCATCGTGATGCTTCTCTGA 159
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Db 332 TGTCTCTTGTGATCTGTATCATCGTGATGCTTCTCTGA 370
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RESULT 34
AL600429
LOCUS
DEFINITION
    AL600429 DKFZp313J1933_r1 313 (synonym: hlcc2) Homo sapiens cDNA clone
    DKFZp313J1933_5", mRNA sequence.
ACCESSION
    AL600429
VERSION
    AL600429.1 GI:15163935
KEYWORDS
    EST.
SOURCE
    Homo sapiens (human)
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ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Hominidae; Homo.
REFERENCE 1 (bases 1 to 552)
AUTHORS Koehrer, K., Beyer, A., Mewes, W., Weil, B. and Wiemann, S.
TITLE EST (Koehrer, K., Beyer, A., Mewes, W., Weil, B. and Wiemann, S.)
JOURNAL Unpublished (1999)
COMMENT Contact: MIPS
MIPS
Ingolstaedter Landstr.1, D-85764 Neuherberg, Germany
This is the 5' sequence of the clone insert
Clone from S. Wiemann, Molecular Genome Analysis, German Cancer
Research Center (DKFZ); Email s.wiemann@dkfz-heidelberg.de;
sequenced by BMPZ (Biomedical Research Center at the Charite,
Berlin/Germany) within the cDNA sequencing consortium of the German
Genome Project.
No sl sequence available.
This clone (DKFZp313J1933) is available at the RZPD in Berlin.
Please contact the RZPD: Ressourcenzentrum, Heubnerweg 6, 14059
Berlin-Charlottenburg, GERMANY; Email: clone@rzpd.de.
FEATURES
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QY 1 ATGGAGAAAGTCCAAATACCTCAGCTAGCTATAGAGAGCCCTCAACCATTTGAATG 60
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DB 233 CCTCAACAGCAGCTCAAAAGCTACAGAAATCTATTTATCAATTTCTCTCATCTTAATA 292
QY 121 TGTCTCTTCTGATCTGATCATCGTATCGTCTCTCTGA 159
DB 293 TGTCTCTTCTGATCTGATCATCGTATCGTCTCTCTGA 331
RESULT 35
LOCUS BP259458 552 bp mRNA linear EST 16-SEP-2004
DEFINITION BP259458 Sugano cDNA library, heart Homo sapiens cDNA clone
HRT06808, mRNA sequence.
ACCESSION BP259458
VERSION BP259458.1 GI:52174688
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Hominidae; Homo.
REFERENCE 1 (bases 1 to 552)
AUTHORS Suzuki, Y., Yamashita, R., Shirota, M., Sakakibara, Y., Chiba, J.,
Mizushima-Sugano, J., Nakai, K. and Sugano, S.
TITLE Sequence comparison of human and mouse genes reveals a homologous
block structure in the promoter regions
JOURNAL Genome Res. 14 (9), 1711-1718 (2004)
PUBMED 15342556
COMMENT Contact: Yutaka Suzuki
Department of Virology
Institute of Medical Science, University of Tokyo
4-6-1, Shirokanedai, Minatoku, Tokyo 108-8639, Japan
Email: ysuzuki@ims.u-tokyo.ac.jp.
FEATURES
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Best Local Similarity 100.0%; Pred. No. 8.7e-35;
Matches 159; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 ATGGAGAAAGTCCAAATACCTCAGCTAGCTATAGAGAGCCCTCAACCATTTGAATG 60
DB 195 ATGGAGAAAGTCCAAATACCTCAGCTAGCTATAGAGAGCCCTCAACCATTTGAATG 254

Institute of Medical Science, University of Tokyo
4-6-1, Shirokanedai, Minatoku, Tokyo 108-8639, Japan
Email: ysuzuki@ims.u-tokyo.ac.jp.
FEATURES
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Best Local Similarity 100.0%; Pred. No. 8.7e-35;
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QY 1 ATGGAGAAAGTCCAAATACCTCAGCTAGCTATAGAGAGCCCTCAACCATTTGAATG 60
DB 181 ATGGAGAAAGTCCAAATACCTCAGCTAGCTATAGAGAGCCCTCAACCATTTGAATG 240
QY 61 CCTCAACAGCAGCTCAAAAGCTACAGAAATCTATTTATCAATTTCTCTCATCTTAATA 120
DB 241 CCTCAACAGCAGCTCAAAAGCTACAGAAATCTATTTATCAATTTCTCTCATCTTAATA 300
QY 121 TGTCTCTTCTGATCTGATCATCGTATCGTCTCTCTGA 159
DB 301 TGTCTCTTCTGATCTGATCATCGTATCGTCTCTCTGA 339
RESULT 36
LOCUS BP257543 553 bp mRNA linear EST 16-SEP-2004
DEFINITION BP257543 Sugano cDNA library, heart Homo sapiens cDNA clone
HRT01211, mRNA sequence.
ACCESSION BP257543
VERSION BP257543.1 GI:52172773
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Hominidae; Homo.
REFERENCE 1 (bases 1 to 553)
AUTHORS Suzuki, Y., Yamashita, R., Shirota, M., Sakakibara, Y., Chiba, J.,
Mizushima-Sugano, J., Nakai, K. and Sugano, S.
TITLE Sequence comparison of human and mouse genes reveals a homologous
block structure in the promoter regions
JOURNAL Genome Res. 14 (9), 1711-1718 (2004)
PUBMED 15342556
COMMENT Contact: Yutaka Suzuki
Department of Virology
Institute of Medical Science, University of Tokyo
4-6-1, Shirokanedai, Minatoku, Tokyo 108-8639, Japan
Email: ysuzuki@ims.u-tokyo.ac.jp.
FEATURES
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Best Local Similarity 100.0%; Pred. No. 8.7e-35;
Matches 159; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 ATGGAGAAAGTCCAAATACCTCAGCTAGCTATAGAGAGCCCTCAACCATTTGAATG 60
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QY 61 CCTCAACAGCAGCTCAAAAGCTACAGAACTCTATTATCAATTTCTGTCTCATCTTAATA 120
Db 255 CCTCAACAGCAGCTCAAAAGCTACAGAACTCTATTATCAATTTCTGTCTCATCTTAATA 314

QY 121 TGTCTCTTGTCTGATCTGTATCATCGTGATGCTTCTCTGA 159
Db 315 TGTCTCTTGTCTGATCTGTATCATCGTGATGCTTCTCTGA 353

RESULT 37
BP258625 Sugano cDNA library, heart Homo sapiens cDNA clone EST 16-SEP-2004
LOCUS HRT04008, mRNA sequence.
DEFINITION
ACCESSION BP258625
VERSION BP258625.1 GI:52173855
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Hominidae; Homo.
1 (bases 1 to 554)
Suzuki,Y., Yamashita,R., Shirota,M., Sakakibara,Y., Chiba,J.,
Mizushima-Sugano,J., Nakai,K. and Sugano,S.
Sequence comparison of human and mouse genes reveals a homologous
block structure in the promoter regions
Genome Res. 14 (9), 1711-1718 (2004)
15342556
Contact: Yutaka Suzuki
Department of Virology
Institute of Medical Science, University of Tokyo
4-6-1, Shirokanedai, Minatoku, Tokyo 108-8639, Japan
Email: ysuzuki@ims.u-tokyo.ac.jp.

FEATURES
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QY 61 CCTCAACAGCAGCTCAAAAGCTACAGAACTCTATTATCAATTTCTGTCTCATCTTAATA 120
Db 255 CCTCAACAGCAGCTCAAAAGCTACAGAACTCTATTATCAATTTCTGTCTCATCTTAATA 314

QY 121 TGTCTCTTGTCTGATCTGTATCATCGTGATGCTTCTCTGA 159
Db 315 TGTCTCTTGTCTGATCTGTATCATCGTGATGCTTCTCTGA 353

RESULT 38
BP257310 Sugano cDNA library, heart Homo sapiens cDNA clone EST 16-SEP-2004
LOCUS HRT00632, mRNA sequence.
DEFINITION
ACCESSION BP257310
VERSION BP257310.1 GI:52172540
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;

Hominidae; Homo.
1 (bases 1 to 556)
Suzuki,Y., Yamashita,R., Shirota,M., Sakakibara,Y., Chiba,J.,
Mizushima-Sugano,J., Nakai,K. and Sugano,S.
Sequence comparison of human and mouse genes reveals a homologous
block structure in the promoter regions
Genome Res. 14 (9), 1711-1718 (2004)
15342556
Contact: Yutaka Suzuki
Department of Virology
Institute of Medical Science, University of Tokyo
4-6-1, Shirokanedai, Minatoku, Tokyo 108-8639, Japan
Email: ysuzuki@ims.u-tokyo.ac.jp.

FEATURES
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/tissue_type="heart"
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QY 121 TGTCTCTTGTCTGATCTGTATCATCGTGATGCTTCTCTGA 159
Db 315 TGTCTCTTGTCTGATCTGTATCATCGTGATGCTTCTCTGA 353

RESULT 39
BP258394 Sugano cDNA library, heart Homo sapiens cDNA clone EST 16-SEP-2004
LOCUS HRT03359, mRNA sequence.
DEFINITION
ACCESSION BP258394
VERSION BP258394.1 GI:52173624
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Hominidae; Homo.
1 (bases 1 to 558)
Suzuki,Y., Yamashita,R., Shirota,M., Sakakibara,Y., Chiba,J.,
Mizushima-Sugano,J., Nakai,K. and Sugano,S.
Sequence comparison of human and mouse genes reveals a homologous
block structure in the promoter regions
Genome Res. 14 (9), 1711-1718 (2004)
15342556
Contact: Yutaka Suzuki
Department of Virology
Institute of Medical Science, University of Tokyo
4-6-1, Shirokanedai, Minatoku, Tokyo 108-8639, Japan
Email: ysuzuki@ims.u-tokyo.ac.jp.

FEATURES
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LOCUS AI720214 559 bp mRNA linear EST 10-JUN-1999

DEFINITION ab94805.x1 Barstead colon HPLRB7 Homo sapiens cDNA clone IMAGE:2335376 3' similar to gb:M63603 CARDIAC PHOSPHOLAMBAN (HUMAN); mRNA sequence.

ACCESSION AI720214

VERSION AI720214.1 GI:5037470

KEYWORDS EST.

SOURCE Homo sapiens (human)

ORGANISM Homo sapiens

REFERENCE 1 (bases 1 to 559)

AUTHORS Hillier,L., Allen,M., Bowles,L., Dubuque,T., Geisel,G., Jost,S., Krizman,D., Kuback,T., Lacy,M., Le,N., Lennon,G., Marra,M., Martin,J., Moore,B., Schellenberg,K., Steptoe,M., Tan,P., Theising,B., White,Y., Wylie,T., Waterston,R. and Wilson,R.

TITLE WashU-NCI human EST Project

JOURNAL Unpublished (1997)

COMMENT Contact: Wilson RK
Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
Tel: 314 286 1800
Fax: 314 286 1810
Email: est@watson.wustl.edu

FEATURES

Source

1..559

/organism="Homo sapiens"

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/sex="male"

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/clone_lib="Barstead colon HPLRB7"

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ORIGIN

Query Match 100.0%; Score 159; DB 1; Length 559;
Best Local Similarity 100.0%; Pred. No. 8.7e-35;
Matches 159; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ATGAGAGAAGTCCAAATACCTCACTCGCTCAGCTATAGAAGAGCCCTCAACCATTTGAAATG 60

Db 418 ATGAGAGAAGTCCAAATACCTCACTCGCTCAGCTATAGAAGAGCCCTCAACCATTTGAAATG 359

QY 61 CCTCAACAGACGCTCAAAAGCTACAGAACTCTATTTATCAATTTCTGCTCATCTTAATA 120

Db 358 CCTCAACAGACGCTCAAAAGCTACAGAACTCTATTTATCAATTTCTGCTCATCTTAATA 299

QY 121 TGTCTCTTGTGATCTGTATCATCGTATGCTTCTCTGA 159

Db 298 TGTCTCTTGTGATCTGTATCATCGTATGCTTCTCTGA 260

RESULT 42

LOCUS BP260265

DEFINITION BP260265 Sugano cDNA library, heart Homo sapiens cDNA clone HRT09360, mRNA sequence.

ACCESSION BP260265

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ORIGIN
Query Match      100.0%; Score 159; DB 3; Length 558;
Best Local Similarity 100.0%; Pred. No. 8.7e-35;
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QY      61  CCTCAACAAGCAGCTCAAAAGCTACAGACTATTAATCAATTTCTGTCTCATCTTAATA 120
DB      255 CCTCAACAAGCAGCTCAAAAGCTACAGACTATTAATCAATTTCTGTCTCATCTTAATA 314

QY      121 TGTCTCTTGTGATCTGTATCATCGTGCATCTTCTCTGA 159
DB      315 TGTCTCTTGTGATCTGTATCATCGTGCATCTTCTCTGA 353

RESULT 40
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LOCUS            BP258989 Sugano cDNA library, heart Homo sapiens cDNA clone
DEFINITION      HRT05216, mRNA sequence.
ACCESSION      BP258989
VERSION        BP258989.1 GI:52174219
KEYWORDS       EST.
SOURCE         Homo sapiens (human)
ORGANISM       Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Hominoidea; Homo.
REFERENCE      1 (bases 1 to 558)
AUTHORS       Suzuki, Y., Yamashita, R., Shirota, M., Sakakibara, Y., Chiba, J.,
Mizushima-Sugano, J., Nakai, K. and Sugano, S.
TITLE         Sequence comparison of human and mouse genes reveals a homologous
              block structure in the promoter regions
JOURNAL        Genome Res. 14 (9), 1711-1718 (2004)
PUBMED        15342556
COMMENT        Contact: Yutaka Suzuki
              Department of Virology
              Institute of Medical Science, University of Tokyo
              4-6-1, Shirokanedai, Minatoku, Tokyo 108-8639, Japan
              Email: yusuzuki@ims.u-tokyo.ac.jp.
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QY      1  ATGGAGAAAGTCCAAATACCTCAGCTCGCTACAGACTATAAGAGAGCCTCAACCAATTGAAATG 60
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QY      61  CCTCAACAAGCAGCTCAAAAGCTACAGACTATTAATCAATTTCTGTCTCATCTTAATA 120
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QY      121 TGTCTCTTGTGATCTGTATCATCGTGCATCTTCTCTGA 159
DB      316 TGTCTCTTGTGATCTGTATCATCGTGCATCTTCTCTGA 354

RESULT 41
AI720214/c

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VERSION BP260265.1 GI:52175496
SOURCE EST.
ORGANISM Homo sapiens (human)

REFERENCE
AUTHORS Suzuki,Y., Yamashita,R., Shirota,M., Sakakibara,Y., Chiba,J.,
Mizushima-Sugano,J., Nakai,K. and Sugano,S.
TITLE Sequence comparison of human and mouse genes reveals a homologous
block structure in the promoter regions
JOURNAL Genome Res. 14 (9), 1711-1718 (2004)
PUBMED 15342556
COMMENT Contact: Yutaka Suzuki
Department of Virology
Institute of Medical Science, University of Tokyo
4-6-1, Shirokanedai, Minatoku, Tokyo 108-8639, Japan
Email: yusuzuki@ims.u-tokyo.ac.jp.

FEATURES
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Best Local Similarity 100.0%; Pred. No. 8.7e-35;
Matches 159; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ATGGAGAAAGTCAATACCTCTCGCTCAGCTATAGAAGAGCCTCAACATTGAAATG 60
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QY 121 TGTCTCTTGTGATCTGTATCATCGTGATGCTTCTCTGA 159
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RESULT 43
BP257291 Sugano cdna library, heart Homo sapiens EST 16-SEP-2004
LOCUS HRT00595, mRNA sequence.
DEFINITION
ACCESSION BP257291
VERSION BP257291.1 GI:52172521
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Hominidae; Homo.
REFERENCE
1 (bases 1 to 560)
Suzuki,Y., Yamashita,R., Shirota,M., Sakakibara,Y., Chiba,J.,
Mizushima-Sugano,J., Nakai,K. and Sugano,S.
TITLE Sequence comparison of human and mouse genes reveals a homologous
block structure in the promoter regions
JOURNAL Genome Res. 14 (9), 1711-1718 (2004)
PUBMED 15342556
COMMENT Contact: Yutaka Suzuki
Department of Virology
Institute of Medical Science, University of Tokyo
4-6-1, Shirokanedai, Minatoku, Tokyo 108-8639, Japan
Email: yusuzuki@ims.u-tokyo.ac.jp.
Location/Qualifiers
1..560

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1..561
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DB 264 CCTCAACAGCAGCTCAAAAGCTACAGATCTATTATCAATTTCTGCTCATCTTAATA 323
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QY 121 TGTCTCTTGTGATCTGTATCATCGTGATGCTTCTCTGA 159
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DB 324 TGTCTCTTGTGATCTGTATCATCGTGATGCTTCTCTGA 362
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RESULT 44
AL600477 561 bp mRNA linear EST 04-SEP-2003
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DEFINITION
ACCESSION AL600477
VERSION AL600477.1 GI:15163983
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Hominidae; Homo.
REFERENCE
1 (bases 1 to 561)
Koehler,K., Beyer,A., Mewes,H.W., Weil,B. and Wiemann,S.
AUTHORS EST (Koehler,K., Beyer,A., Mewes,H.W., Weil,B. and Wiemann,S.)
TITLE Unpublished (1999)
JOURNAL
COMMENT Contact: MIPS
MIPS
Ingolstaedter Landstr.1, D-85764 Neuherberg, Germany
This is the 5' sequence of the clone insert
Clone from S. Wiemann, Molecular Genome Analysis, German Cancer
Research Center (DKFZ); Email s.wiemann@dkfz-heidelberg.de;
sequenced by BMFZ (Biomedical Research Center at the Charite,
Berlin/Germany) within the cdna sequencing consortium of the German
Genome Project.
No sl sequence available.
This clone (DKFp313N2433) is available at the RZPD in Berlin.
Please contact the RZPD: Ressourcenzentrum, Heubnerweg 6, 14059
Berlin-Charlottenburg, GERMANY; Email: clone@rzpd.de.

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Qy 121 TGTCTCTTCTGCTGATCTGATCATCATCGTATGCTTCTCTGA 159

Db 302 TGTCTCTTCTGCTGATCTGATCATCATCGTATGCTTCTCTGA 340

RESULT 45

LOCUS BP257982

DEFINITION BP257982 Sugano cDNA library, heart Homo sapiens cDNA clone

ACCESSION HRT02342, mRNA sequence.

VERSION BP257982

KEYWORDS EST.

SOURCE BP257982.1 GI:52173212

ORGANISM Homo sapiens (human)

REFERENCE Suzuki, Y., Yamashita, R., Shiota, M., Sakakibara, Y., Chiba, J., Mizushima-Sugano, J., Nakai, K. and Sugano, S. Sequence comparison of human and mouse genes reveals a homologous block structure in the promoter regions Genome Res. 14 (9), 1711-1718 (2004)

JOURNAL 15342556

PUBMED

COMMENT Contact: Yutaka Suzuki
Department of Virology
Institute of Medical Science, University of Tokyo
4-6-1, Shirokanedai, Minatoku, Tokyo 108-8639, Japan
Email: yusuzuki@ims.u-tokyo.ac.jp.

FEATURES

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Qy 121 TGTCTCTTCTGCTGATCTGATCATCATCGTATGCTTCTCTGA 159

Db 304 TGTCTCTTCTGCTGATCTGATCATCATCGTATGCTTCTCTGA 342

RESULT 46

LOCUS BP258939

DEFINITION BP258939 Sugano cDNA library, heart Homo sapiens cDNA clone

ACCESSION HRT05022, mRNA sequence.

VERSION BP258939

KEYWORDS EST.

SOURCE BP258939.1 GI:52174169

ORGANISM Homo sapiens (human)

REFERENCE Suzuki, Y., Yamashita, R., Shiota, M., Sakakibara, Y., Chiba, J., Mizushima-Sugano, J., Nakai, K. and Sugano, S. Sequence comparison of human and mouse genes reveals a homologous block structure in the promoter regions Genome Res. 14 (9), 1711-1718 (2004)

JOURNAL 15342556

PUBMED

COMMENT Contact: Yutaka Suzuki
Department of Virology
Institute of Medical Science, University of Tokyo
4-6-1, Shirokanedai, Minatoku, Tokyo 108-8639, Japan
Email: yusuzuki@ims.u-tokyo.ac.jp.

FEATURES

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Db 304 TGTCTCTTCTGCTGATCTGATCATCATCGTATGCTTCTCTGA 342

RESULT 47

LOCUS BP257744

DEFINITION BP257744 Sugano cDNA library, heart Homo sapiens cDNA clone

ACCESSION HRT01757, mRNA sequence.

VERSION BP257744

KEYWORDS EST.

SOURCE BP257744.1 GI:52172974

ORGANISM Homo sapiens (human)

REFERENCE Suzuki, Y., Yamashita, R., Shiota, M., Sakakibara, Y., Chiba, J., Mizushima-Sugano, J., Nakai, K. and Sugano, S. Sequence comparison of human and mouse genes reveals a homologous block structure in the promoter regions Genome Res. 14 (9), 1711-1718 (2004)

JOURNAL 15342556

PUBMED

COMMENT Contact: Yutaka Suzuki
Department of Virology
Institute of Medical Science, University of Tokyo
4-6-1, Shirokanedai, Minatoku, Tokyo 108-8639, Japan
Email: yusuzuki@ims.u-tokyo.ac.jp.

FEATURES

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ORGANISM Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae; Homo.

REFERENCE 1 (bases 1 to 561)

AUTHORS Suzuki, Y., Yamashita, R., Shiota, M., Sakakibara, Y., Chiba, J., Mizushima-Sugano, J., Nakai, K. and Sugano, S.

TITLE Sequence comparison of human and mouse genes reveals a homologous block structure in the promoter regions

JOURNAL Genome Res. 14 (9), 1711-1718 (2004)

PUBMED 15342556

COMMENT Contact: Yutaka Suzuki
Department of Virology
Institute of Medical Science, University of Tokyo
4-6-1, Shirokanedai, Minatoku, Tokyo 108-8639, Japan
Email: yusuzuki@ims.u-tokyo.ac.jp.

FEATURES

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Db 256 CCTCAACAGCAGCTCAAAAGCTACAGAAATCTATTATCAATTTCTGCTCATCTTAATA 315

Qy 121 TGTCTCTTCTGCTGATCTGATCATCATCGTATGCTTCTCTGA 159

Db 316 TGTCTCTTCTGCTGATCTGATCATCATCGTATGCTTCTCTGA 354

ORGANISM Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae; Homo.

REFERENCE 1 (bases 1 to 561)

AUTHORS Suzuki, Y., Yamashita, R., Shiota, M., Sakakibara, Y., Chiba, J., Mizushima-Sugano, J., Nakai, K. and Sugano, S.

TITLE Sequence comparison of human and mouse genes reveals a homologous block structure in the promoter regions

JOURNAL Genome Res. 14 (9), 1711-1718 (2004)

PUBMED 15342556

COMMENT Contact: Yutaka Suzuki
Department of Virology
Institute of Medical Science, University of Tokyo
4-6-1, Shirokanedai, Minatoku, Tokyo 108-8639, Japan
Email: yusuzuki@ims.u-tokyo.ac.jp.

FEATURES

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Qy 61 CCTCAACAGCAGCTCAAAAGCTACAGAAATCTATTATCAATTTCTGCTCATCTTAATA 120

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Qy 121 TGTCTCTTCTGCTGATCTGATCATCATCGTATGCTTCTCTGA 159

Db 316 TGTCTCTTCTGCTGATCTGATCATCATCGTATGCTTCTCTGA 354

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ACCESSION HRT00770, mRNA sequence.
VERSION BP257372.1 GI:52172602
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SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Hominidae; Homo.
REFERENCE 1 (bases 1 to 563)
AUTHORS Suzuki,Y., Yamashita,R., Shiota,M., Sakakibara,Y., Chiba,J.,
Mizushima-Sugano,J., Nakai,K. and Sugano,S.
TITLE Sequence comparison of human and mouse genes reveals a homologous
block structure in the promoter regions
JOURNAL Genome Res. 14 (9), 1711-1718 (2004)
PUBMED 15342556
COMMENT Contact: Yutaka Suzuki
Department of Virology
Institute of Medical Science, University of Tokyo
4-6-1, Shirokanedai, Minatoku, Tokyo 108-8639, Japan
Email: ysuzuki@ims.u-tokyo.ac.jp.
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DEFINITION BP257855 Sugano cDNA library, heart Homo sapiens cDNA clone
ACCESSION HRT02035, mRNA sequence.
VERSION BP257855.1 GI:52173085
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SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Hominidae; Homo.
REFERENCE 1 (bases 1 to 563)
AUTHORS Suzuki,Y., Yamashita,R., Shiota,M., Sakakibara,Y., Chiba,J.,
Mizushima-Sugano,J., Nakai,K. and Sugano,S.
TITLE Sequence comparison of human and mouse genes reveals a homologous
block structure in the promoter regions
JOURNAL Genome Res. 14 (9), 1711-1718 (2004)
PUBMED 15342556
COMMENT Contact: Yutaka Suzuki
Department of Virology
Institute of Medical Science, University of Tokyo
4-6-1, Shirokanedai, Minatoku, Tokyo 108-8639, Japan
Email: ysuzuki@ims.u-tokyo.ac.jp.
FEATURES
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```

COMMENT

Contact: Yutaka Suzuki
Department of Virology
Institute of Medical Science, University of Tokyo
4-6-1, Shirokanedai, Minatoku, Tokyo 108-8639, Japan
Email: yuzuki@ims.u-tokyo.ac.jp

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